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OM protein - protein search, using sw model

Run on: January 6, 2003, 11:18:45 ; Search time 36 Seconds
(without alignments)
142.663 Million cell updates/sec

Title: US-09-936-024-1

Perfect score: 1491
Sequence: 1 VAEPTYPWDAETGERLVC.....RVARMGLERSYVERFLPVH 271

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 117078 seqs, 18951520 residues

Total number of hits satisfying chosen parameters: 117078

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications_AA:*
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2: /cgn2_6/ptodata/2/pubppaa/PCT_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	1491	100.0	300	10	US-09-896-096A-1
2	1491	100.0	300	10	US-09-894-924-1
3	1491	100.0	300	10	US-09-935-727-2
4	1476.5	99.0	289	10	US-09-877-156-17
5	1469	98.5	300	10	US-09-840-795-2
6	1034	69.3	211	10	US-09-877-156-20
7	841	56.4	153	10	US-09-877-156-2
8	671	45.0	170	10	US-09-935-727-4
9	461	30.9	126	10	US-09-062-113-71
10	442.5	29.7	401	10	US-09-062-113-62
11	440.5	29.5	272	10	US-09-062-113-75
12	440.5	29.5	293	10	US-09-896-096A-18
13	440.5	29.5	321	10	US-09-894-924-18
14	440.5	29.5	321	10	US-09-062-113-80
15	440.5	29.5	327	10	US-09-062-113-72
16	440.5	29.5	351	10	US-09-062-113-74
17	440.5	29.5	362	10	US-09-062-113-11
18	440.5	29.5	380	10	US-09-062-113-4
19	440.5	29.5	391	10	US-09-062-113-106

20	440.5	29.5	393	10	US-09-062-113-79	Sequence 79, Appl
21	440.5	29.5	399	10	US-09-062-113-73	Sequence 73, Appl
22	440.5	29.5	401	10	US-09-062-113-5	Sequence 5, Appl
23	440.5	29.5	401	10	US-09-062-113-64	Sequence 64, Appl
24	440.5	29.5	401	10	US-09-062-113-65	Sequence 65, Appl
25	440.5	29.5	401	10	US-09-062-113-66	Sequence 66, Appl
26	440.5	29.5	401	12	US-10-039-785-5	Sequence 1, Appl
27	440.5	29.5	401	12	US-10-066-209-1	Sequence 1, Appl
28	440.5	29.5	401	12	US-10-164-592-2	Sequence 2, Appl
29	433.5	29.1	401	10	US-09-062-113-63	Sequence 63, Appl
30	433	29.0	187	10	US-09-062-113-81	Sequence 81, Appl
31	433	29.0	187	10	US-09-840-795-11	Sequence 11, Appl
32	433	29.0	197	10	US-09-062-113-76	Sequence 76, Appl
33	432	29.0	394	10	US-09-062-113-9	Sequence 9, Appl
34	407	27.3	147	9	US-09-756-854-20	Sequence 20, Appl
35	407	27.3	147	9	US-10-041-574-20	Sequence 20, Appl
36	356.5	23.9	360	10	US-09-062-113-67	Sequence 67, Appl
37	342.5	23.0	450	10	US-09-768-779A-3	Sequence 3, Appl
38	342.5	23.0	461	10	US-09-826-212-4	Sequence 4, Appl
39	342.5	23.0	461	10	US-09-896-096A-17	Sequence 17, Appl
40	342.5	23.0	461	10	US-09-894-924-17	Sequence 17, Appl
41	342.5	23.0	461	10	US-09-840-707A-17	Sequence 17, Appl
42	342.5	23.0	461	10	US-09-935-727-6	Sequence 6, Appl
43	340.5	22.8	461	10	US-09-800-909-2	Sequence 2, Appl
44	340.5	22.8	461	10	US-09-758-124-2	Sequence 2, Appl
45	340.5	22.8	461	10	US-09-800-908-3	Sequence 3, Appl

ALIGNMENTS

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RESULT 1
US-09-896-096A-1
; Sequence 1, Application US/09896096A
; Patent No. US2002061559A1
; GENERAL INFORMATION:
; APPLICANT: ASHKENAZI, AVI J
; APPLICANT: BOTSTEIN, DAVID
; APPLICANT: DODGE, KELLY H.
; APPLICANT: GURNEY, AUSTIN L.
; APPLICANT: KIM, KYONG JIN
; APPLICANT: LAWRENCE, DAVID A.
; APPLICANT: PITTI, ROBERT
; APPLICANT: ROY, MARGARET A
; APPLICANT: TUMAS, DANIEL B
; APPLICANT: WOOD, WILLIAM I.
; TITLE OF INVENTION: DcR3 Polypeptide, A TNFR Homolog
; FILE REFERENCE: P134R2 REVISED
; CURRENT APPLICATION NUMBER: US/09/896,096A
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US 09/157,289
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: US 60/059,288
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: US 60/094,640
; PRIOR FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 18
; SEQ ID NO 1
; LENGTH: 300
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-896-096A-1
Query Match      100.0%; Score 1491; DB 10; Length 300;
Best Local Similarity 100.0%; Pred. No. 8.8e-107;
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 VAEPTYPWDAETGERLVCACPPGTFVORPCRRBSPTTCGCPRHRYQFMNLYRCR 60
Db      30 VAEPTYPWDAETGERLVCACPPGTFVORPCRRBSPTTCGCPRHRYQFMNLYRCR 89
QY      61 YCNVLGEREEARACHATINRAACRCRTGFFAHAGFLEHASCPGAGVIAPTPSQNTQ 120
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Db	90	YCNVLCGEREEERACHATNHRACRCTGTFPAHAGFCLEHASCPPGAGVIAPGTTPSQNTQ	149
Qy	121	CQCPPTGTFGASSSSSSQCPHRNCTALGALANVPSSSHDTLTCTGTFPLSTRVPGAE	180
Db	150	CQCPPTGTFGASSSSSSQCPHRNCTALGALANVPSSSHDTLTCTGTFPLSTRVPGAE	209
Qy	181	ECERAVIDFVAFQDISIKRLQRLQALEAPEGPGTTPRAGRAALQKLRRLTELLGAQD	240
Db	210	ECERAVIDFVAFQDISIKRLQRLQALEAPEGPGTTPRAGRAALQKLRRLTELLGAQD	269
Qy	241	GALLVRLQALRVARMPCGLERSVRERFLPVH	271
Db	270	GALLVRLQALRVARMPCGLERSVRERFLPVH	300

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RESULT 2
US-09-894-924-1
; Sequence 1, Application US/09894924
; Patent No. US20020065210A1
; GENERAL INFORMATION:
; APPLICANT: ASHKENAZI, AVI J
; APPLICANT: BOTSTEIN, DAVID
; APPLICANT: DODGE, KELLY H.
; APPLICANT: GURNEY, AUSTIN L.
; APPLICANT: KIM, KYUNG JIN
; APPLICANT: LAWRENCE, DAVID A.
; APPLICANT: PITTI, ROBERT
; APPLICANT: ROY, MARGARET A
; APPLICANT: TUNAS, DANIEL B
; APPLICANT: WOOD, WILLIAM I.
; TITLE OF INVENTION: Dcr3 Polypeptide, A TNFR Homolog
; FILE REFERENCE: P1134R2 REVISED
; CURRENT APPLICATION NUMBER: US/09/894,924
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US 09/157,289
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: US 60/059,288
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: US 60/094,640
; PRIOR FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 18
; SEQ ID NO 1
; LENGTH: 300
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-894-924-1

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RESULT 3

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US-09-935-727-2
; Sequence 2, Application US/09935727
; Patent No. US20020150583A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Tumor Necrosis Factor Receptors 6 Alpha and 6 Beta
; FILE REFERENCE: PP454P2
; CURRENT APPLICATION NUMBER: US/09/935,727
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/303,224
; PRIOR FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: 60/252,131
; PRIOR FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: 60/227,598
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: 09/518,931
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: 60/168,235
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: 60/146,371
; PRIOR FILING DATE: 1999-08-02
; PRIOR APPLICATION NUMBER: 60/131,964
; PRIOR FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: 60/131,270
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/124,092
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/121,774
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: 09/006,352
; PRIOR FILING DATE: 1998-01-13
; PRIOR APPLICATION NUMBER: 60/035,496
; PRIOR FILING DATE: 1997-01-14
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 300
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-727-2

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RESULT 4
US-09-877-156-17
; Sequence 17, Application US/09877156
; Patent No. US20020055625A1
; GENERAL INFORMATION:
; APPLICANT: Catherine Tribouley
; TITLE OF INVENTION: NEW MEMBERS OF TNF AND TNFR FAMILIES

FILE REFERENCE: 1408.003/200130.439C1
CURRENT APPLICATION NUMBER: US/09/877,156
CURRENT FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: US 09/286,529
PRIOR FILING DATE: 1998-04-05
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FaastSeq for Windows Version 3.0
SEQ ID NO 17
LENGTH: 299
TYPE: PRT
ORGANISM: Homo sapien
US-09-877-156-17

Query Match 99.0%; Score 1476.5; DB 10; Length 299;
Best Local Similarity 99.6%; Pred. No. 1,1e-105;
Matches 270; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 VAETPTVPMWDAETGERLVCAQCPGTFVORPCRRDPTTCGCPPHHYTQFMNLYLRCR 60
DB 30 VAETPTVPMWDAETGERLVCAQCPGTFVORPCRRDPTTCGCPPHHYTQFMNLYLRCR 89
QY 61 YCNVLGGEREEERARACHATNRAACRCRTGFFAHAGFCLHASCPCPGAGVIAPTGPSQNTQ 120
DB 90 YCNVLGGEREEERARACHATNRAACRCRTGFFAHAGFCLHASCPCPGAGVIAPTGPSQNTQ 149
QY 121 CQCPGPTFSASSSSBOCQPHRNCTALGLALNVPGSSSHDTLCTGCTGFPPLSTRVPGAE 180
DB 150 CQCPGPTFSASSSSBOCQPHRNCTALGLALNVPGSSSHDTLCTGCTGFPPLSTRVPGAE 208
QY 181 ECERAVIDFAFODISIKRLQRLLOALEAPEGWGPTPRAGAAQLKLRRLTELLGAOD 240
DB 209 ECERAVIDFAFODISIKRLQRLLOALEAPEGWGPTPRAGAAQLKLRRLTELLGAOD 268
QY 241 GALLVRLLOALRVARMPGLERSVREERFLPVH 271
DB 269 GALLVRLLOALRVARMPGLERSVREERFLPVH 299

RESULT 5
US-09-840-795-2
Sequence 2, Application US/09840795
Patent No. US20020143147A1
GENERAL INFORMATION:
APPLICANT: Murphy, Erin E.
APPLICANT: Mattson, Jeanine D.
APPLICANT: Bates, Elizabeth Esther Mary
APPLICANT: Gorman, Daniel M.
APPLICANT: Lebecque, Serge J.E.
TITLE OF INVENTION: Mammalian Genes; Related Reagents
FILE REFERENCE: SF0818X
CURRENT APPLICATION NUMBER: US/09/840,795
CURRENT FILING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: 09/351,777
PRIOR FILING DATE: 1999-07-12
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 300
TYPE: PRT
ORGANISM: primate
FEATURE:
NAME/KEY: misc_feature
LOCATION: (79)
OTHER INFORMATION: Xaa at residue 79 is undetermined.
US-09-840-795-2

Query Match 98.5%; Score 1469; DB 10; Length 300;
Best Local Similarity 98.9%; Pred. No. 4.2e-105;
Matches 266; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 VAETPTVPMWDAETGERLVCAQCPGTFVORPCRRDPTTCGCPPHHYTQFMNLYLRCR 60
DB 30 VAETPTVPMWDAETGERLVCAQCPGTFVORPCRRDPTTCGCPPHHYTQFMNLYLRCR 89

QY 61 YCNVLGGEREEERARACHATNRAACRCRTGFFAHAGFCLHASCPCPGAGVIAPTGPSQNTQ 120
DB 90 YCNVLGGEREEERARACHATNRAACRCRTGFFAHAGFCLHASCPCPGAGVIAPTGPSQNTQ 149
QY 121 CQCPGPTFSASSSSBOCQPHRNCTALGLALNVPGSSSHDTLCTGCTGFPPLSTRVPGAE 180
DB 150 CQCPGPTFSASSSSBOCQPHRNCTALGLALNVPGSSSHDTLCTGCTGFPPLSTRVPGAE 209
QY 181 ECERAVIDFAFODISIKRLQRLLOALEAPEGWGPTPRAGAAQLKLRRLTELLGAOD 240
DB 210 ECERAVIDFAFODISIKRLQRLLOALEAPEGWGPTPRAGAAQLKLRRLTELLGAOD 269
QY 241 GALLVRLLOALRVARMPGLERSVREERFLPVH 271
DB 270 GALLVRLLOALRVARMPGLERSVREERFLPVH 300

RESULT 6
US-09-877-156-20
Sequence 20, Application US/09877156
Patent No. US20020055625A1
GENERAL INFORMATION:
APPLICANT: Catherine Tribouley
TITLE OF INVENTION: NEW MEMBERS OF TNF AND TNFR FAMILIES
FILE REFERENCE: 1408.003/200130.439C1
CURRENT APPLICATION NUMBER: US/09/877,156
CURRENT FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: US 09/286,529
PRIOR FILING DATE: 1998-04-05
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FaastSeq for Windows Version 3.0
SEQ ID NO 20
LENGTH: 211
TYPE: PRT
ORGANISM: Homo sapien
US-09-877-156-20

Query Match 69.3%; Score 1034; DB 10; Length 211;
Best Local Similarity 98.9%; Pred. No. 3.9e-72;
Matches 179; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 VAETPTVPMWDAETGERLVCAQCPGTFVORPCRRDPTTCGCPPHHYTQFMNLYLRCR 60
DB 30 VAETPTVPMWDAETGERLVCAQCPGTFVORPCRRDPTTCGCPPHHYTQFMNLYLRCR 89
QY 61 YCNVLGGEREEERARACHATNRAACRCRTGFFAHAGFCLHASCPCPGAGVIAPTGPSQNTQ 120
DB 90 YCNVLGGEREEERARACHATNRAACRCRTGFFAHAGFCLHASCPCPGAGVIAPTGPSQNTQ 149
QY 121 CQCPGPTFSASSSSBOCQPHRNCTALGLALNVPGSSSHDTLCTGCTGFPPLSTRVPGAE 180
DB 150 CQCPGPTFSASSSSBOCQPHRNCTALGLALNVPGSSSHDTLCTGCTGFPPLSTRVPGAE 209
QY 181 E 181
DB 210 E 210

RESULT 7
US-09-877-156-2
Sequence 2, Application US/09877156
Patent No. US20020055625A1
GENERAL INFORMATION:
APPLICANT: Catherine Tribouley
TITLE OF INVENTION: NEW MEMBERS OF TNF AND TNFR FAMILIES
FILE REFERENCE: 1408.003/200130.439C1
CURRENT APPLICATION NUMBER: US/09/877,156
CURRENT FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: US 09/286,529
PRIOR FILING DATE: 1998-04-05
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FaastSeq for Windows Version 3.0

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; SEQ ID NO 2
; LENGTH: 153
; TYPE: PRT
; ORGANISM: human
US-09-877-156-2

Query Match          56.4%; Score 841; DB 10; Length 153;
Best Local Similarity 100.0%; Pred. No. 1.4e-57;
Matches 153; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 56 LERCYCNVLCGEREEERACHATHNRACRRTGFFAHAGFCLEHASCPPGAGVIADGTP 115
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Db 1 LERCYCNVLCGEREEERACHATHNRACRRTGFFAHAGFCLEHASCPPGAGVIADGTP 60
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QY 116 SONTQCPCPPGTFSSASSSEQCQPHRNTALGLALNVPGSSHDLTCTSGTFPLSTR 175
      |||
Db 61 SONTQCPCPPGTFSSASSSEQCQPHRNTALGLALNVPGSSHDLTCTSGTFPLSTR 120
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QY 176 VPGAEECERAVIDFVAFQDISIKRLQRLQALE 208
      |||
Db 121 VPGAEECERAVIDFVAFQDISIKRLQRLQALE 153
      |||

RESULT 8
US-09-935-727-4
; Sequence 4, Application US/09935727
; Patent No. US20020150583A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Tumor Necrosis Factor Receptors 6 Alpha and 6 Beta
; FILE REFERENCE: PF454P2
; CURRENT APPLICATION NUMBER: US/09/935,727
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/303,224
; PRIOR FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: 60/252,131
; PRIOR FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: 60/227,598
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: 09/518,931
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: 60/168,235
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: 60/146,371
; PRIOR FILING DATE: 1999-08-02
; PRIOR APPLICATION NUMBER: 60/131,964
; PRIOR FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: 60/131,270
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/124,092
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/121,774
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: 09/006,352
; PRIOR FILING DATE: 1998-01-13
; PRIOR APPLICATION NUMBER: 60/035,496
; PRIOR FILING DATE: 1997-01-14
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-727-4

Query Match          45.0%; Score 671; DB 10; Length 170;
Best Local Similarity 100.0%; Pred. No. 1.4e-44;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VAETPTYPWRDAETGERLVCACQCPGTFVQPCRRDSPTTCGPPRRHYTFQWNYLERCR 60
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Db 30 VAETPTYPWRDAETGERLVCACQCPGTFVQPCRRDSPTTCGPPRRHYTFQWNYLERCR 89
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QY 61 YCNVLCGEREEERACHATHNRACRRTGFFAHAGFCLEHASCPPGAGVIADG 113
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Db 90 YCNVLCGEREEERACHATHNRACRRTGFFAHAGFCLEHASCPPGAGVIADG 142
      |||

RESULT 9
US-09-062-113-71
; Sequence 71, Application US/09062113
; Patent No. US20020051969A1
; GENERAL INFORMATION:
; APPLICANT: GOTO, Masaaki
; APPLICANT: TSUDA, Eisuke
; APPLICANT: MOCHIZUKI, Shin'ichi
; APPLICANT: YANO, Kazuki
; APPLICANT: KOBAYASHI, Fumie
; APPLICANT: SHIMA, NO. US20020051969A1uyuki
; APPLICANT: YASUDA, Hisataka
; APPLICANT: NAKAGAWA, NO. US20020051969A1uaki
; APPLICANT: MORINAGA, Tomonori
; APPLICANT: UEDA, Masatsugu
; APPLICANT: HIGASHIO, Kanji
; TITLE OF INVENTION: No. US20020051969A1e1 Proteins and Methods for Producing
; TITLE OF INVENTION: the Proteins
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Tesca, Hurwitz & Thibeault
; STREET: 125 High St.
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/062,113
; FILING DATE: 17-APR-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 54977/1995
; FILING DATE: 20-FEB-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 207508/1995
; FILING DATE: 21-JUL-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP96/00374
; FILING DATE: 20-FEB-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/915,004
; FILING DATE: 20-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: MOORE, Ronda P.
; REGISTRATION NUMBER: 44,244
; REFERENCE/DOCKET NUMBER: FJN-060DV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 71:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 326 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: -21..0
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..305
; OTHER INFORMATION: /note= "OCIF-DDD1"
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/062,113
FILING DATE: 17-APR-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 54977/1995
FILING DATE: 20-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 207508/1995
FILING DATE: 21-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/00374
FILING DATE: 20-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,004
FILING DATE: 20-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: MOORE, Ronda P.
REGISTRATION NUMBER: 44,244
REFERENCE/DOCKET NUMBER: FJN-060DV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 75:
SEQUENCE CHARACTERISTICS:
LENGTH: 272 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Peptide
LOCATION: -21..0
FEATURE:
NAME/KEY: Protein
LOCATION: 1..251
OTHER INFORMATION: /note= "OCIF-CDD2"
US-09-062-113-75

Query Match 29.5%; Score 440.5; DB 10; Length 272;
Best Local Similarity 41.2%; Pred. No. 8.5e-27;
Matches 77; Conservative 31; Mismatches 74; Indels 5; Gaps 2;

QY 5 PTPWRDAETGERLVCAQCPGTFVORPCRRDSPPTCGPCPPRHVYTFQWNYLRCRYCNV 64
DB 26 PKYLHYDEETSHQLLCKCPGTYLKQHCTAKWKTVCAPCPDHYTDSWHTSDECLYCSP 85

QY 65 LCGREERAEARACHATHNRACRRTGFFAHAGFCLEHASCPGAGVIAFGTPSQNTQOCPC 124
DB 86 VKELQVVKQECNTHNRVCEKGRYLEIEFCLKHSRCPGPGVQAGTPERNTVCKRC 145

QY 125 PPGTFSSASSSSQCPHRNCTALGLALNVGSSSHDTLCTSCGFPPLSTRVPGAEE--C 182
DB 146 PDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNI---CSGNSESTQKCGIDVTLC 202

QY 183 ERAVIDF 189
DB 203 EEAFFRF 209

RESULT 12
US-09-896-096A-18
Sequence 18; Application US/09896096A
Patent No. US20020061559A1
GENERAL INFORMATION:
APPLICANT: ASHKENAZI, AVI J
APPLICANT: BOTSTEIN, DAVID
APPLICANT: DODGE, KELLY H.
APPLICANT: GURNEY, AUSTIN L.
APPLICANT: KIM, KYUNG JIN
APPLICANT: LAWRENCE, DAVID A.
APPLICANT: PITTI, ROBERT
APPLICANT: ROY, MARGARET A
APPLICANT: TOMAS, DANIEL B
APPLICANT: WOOD, WILLIAM I.
TITLE OF INVENTION: Dcr3 Polypeptide, A TNFR Homolog
FILE REFERENCE: P1134R2 REVISED
CURRENT FILING DATE: 2001-06-28
PRIOR APPLICATION NUMBER: US 09/157,289
PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: US 60/059,288
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: US 60/094,640
PRIOR FILING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 18
SEQ ID NO 18
LENGTH: 293
TYPE: PRT
ORGANISM: Homo sapiens

APPLICANT: LAWRENCE, DAVID A.
APPLICANT: PITTI, ROBERT
APPLICANT: ROY, MARGARET A
APPLICANT: TOMAS, DANIEL B
APPLICANT: WOOD, WILLIAM I.
TITLE OF INVENTION: Dcr3 Polypeptide, A TNFR Homolog
FILE REFERENCE: P1134R2 REVISED
CURRENT APPLICATION NUMBER: US/09/896,096A
CURRENT FILING DATE: 2001-06-28
PRIOR APPLICATION NUMBER: US 09/157,289
PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: US 60/059,288
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: US 60/094,640
PRIOR FILING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 18
SEQ ID NO 18
LENGTH: 293
TYPE: PRT
ORGANISM: Homo sapiens
US-09-896-096A-18

Query Match 29.5%; Score 440.5; DB 10; Length 293;
Best Local Similarity 41.2%; Pred. No. 9.2e-27;
Matches 77; Conservative 31; Mismatches 74; Indels 5; Gaps 2;

QY 5 PTPWRDAETGERLVCAQCPGTFVORPCRRDSPPTCGPCPPRHVYTFQWNYLRCRYCNV 64
DB 26 PKYLHYDEETSHQLLCKCPGTYLKQHCTAKWKTVCAPCPDHYTDSWHTSDECLYCSP 85

QY 65 LCGREERAEARACHATHNRACRRTGFFAHAGFCLEHASCPGAGVIAFGTPSQNTQOCPC 124
DB 86 VKELQVVKQECNTHNRVCEKGRYLEIEFCLKHSRCPGPGVQAGTPERNTVCKRC 145

QY 125 PPGTFSSASSSSQCPHRNCTALGLALNVGSSSHDTLCTSCGFPPLSTRVPGAEE--C 182
DB 146 PDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNI---CSGNSESTQKCGIDVTLC 202

QY 183 ERAVIDF 189
DB 203 EEAFFRF 209

RESULT 13
US-09-894-924-18
Sequence 18; Application US/09894924
Patent No. US20020065210A1
GENERAL INFORMATION:
APPLICANT: ASHKENAZI, AVI J
APPLICANT: BOTSTEIN, DAVID
APPLICANT: DODGE, KELLY H.
APPLICANT: GURNEY, AUSTIN L.
APPLICANT: KIM, KYUNG JIN
APPLICANT: LAWRENCE, DAVID A.
APPLICANT: PITTI, ROBERT
APPLICANT: ROY, MARGARET A
APPLICANT: TOMAS, DANIEL B
APPLICANT: WOOD, WILLIAM I.
TITLE OF INVENTION: Dcr3 Polypeptide, A TNFR Homolog
FILE REFERENCE: P1134R2 REVISED
CURRENT FILING DATE: 2001-06-28
PRIOR APPLICATION NUMBER: US 09/157,289
PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: US 60/059,288
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: US 60/094,640
PRIOR FILING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 18
SEQ ID NO 18
LENGTH: 293
TYPE: PRT
ORGANISM: Homo sapiens

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 6, 2003, 11:15:31 ; Search time 61 Seconds
(without alignments)
591.982 Million cell updates/sec

Title: US-09-936-024-1
Perfect score: 1491
Sequence: 1 VAETPTYPWRDAETGERTLCV.....RVARMPGLERSVREPLPVH 271

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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23: /SIDS2/gcgdata/genseq/genseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1491	100.0	271	20	AA42184 Human mFLINT #1 pr
2	1491	100.0	271	21	AA19334 A mature human FAS
3	1491	100.0	271	21	AA19705 Human FAS ligand 1
4	1491	100.0	271	21	AA97247 M68 TNF receptor r
5	1491	100.0	271	21	AA96598 Human mature FLINT
6	1491	100.0	271	22	AA80357 Human mature fas l
7	1491	100.0	271	22	AA86804 Amino acid sequenc
8	1491	100.0	271	22	AA86804 Amino acid sequenc
9	1491	100.0	271	22	AA87445 Human FLINT mature
10	1491	100.0	271	23	AA814578 Human mature FLINT

11	1491	100.0	300	19	AA66102 Amino acid sequenc
12	1491	100.0	300	19	AA63622 Human tumour necro
13	1491	100.0	300	20	AAV03099 Human lung TNF-rec
14	1491	100.0	300	20	AA42182 Human FLINT #1 pro
15	1491	100.0	300	20	AA17479 Mammalian tumour n
16	1491	100.0	300	20	AAV06817 Human Dcr3 polypep
17	1491	100.0	300	20	AAW97749 Human tumour necro
18	1491	100.0	300	20	AAW95082 Orphan receptor (H
19	1491	100.0	300	21	AA819335 A full length huma
20	1491	100.0	300	21	AA826559 Human soluble TNF
21	1491	100.0	300	21	AA824057 Human PRO212 prote
22	1491	100.0	300	21	AA834416 Human PRO212 prote
23	1491	100.0	300	21	AA803621 Human Fas ligand 1
24	1491	100.0	300	21	AAV97246 M68 TNF receptor r
25	1491	100.0	300	21	AAV90357 Human tumour necro
26	1491	100.0	300	21	AA824395 Human PRO212 prote
27	1491	100.0	300	21	AAV96596 Human FLINT. Homo
28	1491	100.0	300	22	AAE03568 Human native fas l
29	1491	100.0	300	22	AA874466 Human FLINT native
30	1491	100.0	300	22	AA871754 Human NTR3. Homo
31	1491	100.0	300	22	AA848161 Human PRO212 polyp
32	1491	100.0	300	22	AA850903 Human PRO212 prote
33	1491	100.0	300	23	AAE14579 Human native FLINT
34	1491	100.0	300	23	AAE20848 Human tumour necro
35	1491	100.0	341	22	AA873740 Human colon cancer
36	1487	99.7	271	21	AA819709 Protease-resistant
37	1487	99.7	271	21	AA803571 Human mature fas l
38	1487	99.7	271	22	AA874467 Human FLINT mature
39	1487	99.7	271	23	AAE14581 Human protease-res
40	1486	99.7	271	22	AAE03584 Human mature fas l
41	1486	99.7	271	23	AAE14582 Human protease-res
42	1485	99.6	271	21	AAV96599 Human mature FLINT
43	1485	99.6	271	23	AAE14583 Human protease-res
44	1485	99.6	271	23	AAE14584 Human protease-res
45	1485	99.6	271	23	AAE14586 Human protease-res

ALIGNMENTS

RESULT 1
AA42184
ID AA42184 standard; Protein; 271 AA.
XX
AC AA42184;
XX
DT 17-DEC-1999 (first entry)
XX
DE Human mFLINT #1 protein sequence.
XX
KW Human; FLINT; mFLINT; OPB3; tumour necrosis factor receptor; Fas;
KW apoptosis; inflammation; cancer; diabetes; acute liver failure;
KW sepsis; hepatitis; ischaemia-associated injury; hypercoagulation;
KW reperfusion-associated injury; aplastic anaemia; differentiation;
KW growth; myelodysplastic syndrome; pancytopenic condition;
KW myocardial ischaemia.
XX
OS Homo sapiens.
XX
PN WO950413-A2.
XX
PD 07-OCT-1999.
XX
PF 30-MAR-1999; 99WO-US06797.
XX
PR 30-MAR-1998; 98US-0079856.
XX
PR 20-MAY-1998; 98US-0086074.
XX
PR 09-SEP-1998; 98US-0096643.
XX
PR 17-DEC-1998; 98US-0112577.
XX
PR 18-DEC-1998; 98US-0112703.
XX
PR 18-DEC-1998; 98US-0112933.
XX
PR 22-DEC-1998; 98US-0113407.
XX

PA (ELIL) LILLY & CO ELI.
XX Bumol TF, Dou S, Glasebrook AL, Gould KE, Hale JE, Heuer JG;
PI Hui KY, Khaitonenkov A, Mizrahi J, Na S, Noblitt TW, Reidy CA;
XX Song HY, Wang J, Wu X, Zuckerman SH;
DR WPI: 1999-591319/50.
DR N-PSDB; AA225377.
XX
PT Use of mature FLINT for treating acute liver failure, inflammation,
PT cancer, and diabetes - by prevention of FasL-Fas mediated apoptotic
PT and proinflammatory activity
XX
PS Claim 31; Fig 3; 99pp; English.
XX
CC The present invention describes therapeutic applications of mature FLINT
CC (mFLINT) for use in the treatment of acute liver failure. Mature FLINT
CC (mFLINT), which is a member of the tumour necrosis factor receptor
CC superfamily, is used for treating acute liver failure, inflammation of
CC the liver, abnormal hepatocyte apoptosis, sepsis, a disorder associated
CC with inflammation, hepatitis, abnormal apoptosis, an ischaemia-associated
CC injury or disorder such as hypercoagulation (including use with
CC thrombolytic or anti-thrombolytic agents), reperfusion-associated injury
CC or disorder. Type I diabetes, cancer, cell damage or damage to an
CC innocent bystander tissue that is induced by a chemotherapeutic agent or
CC therapeutic irradiation, treating haematopoietic progenitor cells that
CC have been exposed to therapeutic radiation or chemotherapy, aplastic
CC anaemia, myelodysplastic syndrome or a pancytopenic condition. mFLINT is
CC also used for promoting the growth or differentiation of a haematopoietic
CC progenitor cell or CD34+ cell and preventing damage to a cardiac myocyte
CC resulting from abnormal myocardial ischaemia. The present sequence
CC represents human mFLINT.
XX
SQ Sequence 271 AA;
Query Match 100.0%; Score 1491; DB 20; Length 271;
Best Local Similarity 100.0%; Pred No. 8.5e-115;
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VAETPTYWRDAETGERLVCAQCPGGTFVQRPCRRDSPTTCGPPRRHYTFQWNYLERCR 60
Db 1 VAETPTYWRDAETGERLVCAQCPGGTFVQRPCRRDSPTTCGPPRRHYTFQWNYLERCR 60
QY 61 YCNVLCGEREEERACHATNCRCHTGFPAHAGFCLHASCPCPGAGVIAPGTPSNTQ 120
Db 61 YCNVLCGEREEERACHATNCRCHTGFPAHAGFCLHASCPCPGAGVIAPGTPSNTQ 120
QY 121 CQCPPTGTFASSSSSSQCPHNRCTALGLALNVPGSSSHDTLCTCTGPPPLSTRVPGA 180
Db 121 CQCPPTGTFASSSSSSQCPHNRCTALGLALNVPGSSSHDTLCTCTGPPPLSTRVPGA 180
QY 181 ECERAVIDFVAQDISIKRLQRLQALEAPEGMGPTPRAGRAALQLKRRRLTELLGAQD 240
Db 181 ECERAVIDFVAQDISIKRLQRLQALEAPEGMGPTPRAGRAALQLKRRRLTELLGAQD 240
QY 241 GALLVRLQLALRVARMPLGLRSVRERFLPVH 271
Db 241 GALLVRLQLALRVARMPLGLRSVRERFLPVH 271
RESULT 2
AAB19334
ID AAB19334 standard; Protein; 271 AA.
XX
AC AAB19334;
XX
DT 19-FEB-2001 (first entry)
XX
DE A mature human FAS Ligand Inhibitory Protein (FLINT).
XX
KW Human; FAS Ligand Inhibitory Protein; FLINT; analogue; apoptosis;
KW tumour necrosis factor receptor; acute lung injury; pulmonary fibrosis;
KW acute respiratory distress syndrome; ulcerative colitis,

KW chronic obstructive pulmonary disease; Crohn's disease.
XX
OS Homo sapiens.
PH Key Location/Qualifiers
FT Misc-difference 1 /note= "optionally replaced with Met"
FT Misc-difference 2 /note= "optionally replaced with Asn"
FT Misc-difference 4 /note= "optionally replaced with Ala"
FT Misc-difference 12 /note= "optionally replaced with Asn"
FT Misc-difference 13 /note= "optionally replaced with Asp or Gln"
FT Misc-difference 17 /note= "optionally replaced with Trp"
FT Misc-difference 25 /note= "optionally replaced with Asn"
FT Misc-difference 34 /note= "optionally replaced with Asn"
FT Misc-difference 35 /note= "optionally replaced with Asn"
FT Misc-difference 36 /note= "optionally replaced with Thr"
FT Misc-difference 37 /note= "optionally replaced with Asn or Thr"
FT Misc-difference 38 /note= "optionally replaced with Asn"
FT Misc-difference 53 /note= "optionally replaced with Asp"
FT Misc-difference 63 /note= "optionally replaced with Trp"
FT Misc-difference 67 /note= "optionally replaced with Asp"
FT Misc-difference 69 /note= "optionally replaced with Glu"
FT Misc-difference 75 /note= "optionally replaced with Pro"
FT Misc-difference 82 /note= "optionally replaced with Glu or Thr"
FT Misc-difference 88 /note= "optionally replaced with Pro"
FT Misc-difference 94 /note= "optionally replaced with Tyr"
FT Misc-difference 95 /note= "optionally replaced with Asp"
FT Misc-difference 96 /note= "optionally replaced with Gln"
FT Misc-difference 101 /note= "optionally replaced with Thr"
FT Misc-difference 102 /note= "optionally replaced with Leu"
FT Misc-difference 104 /note= "optionally replaced with Ser"
FT Misc-difference 107 /note= "optionally replaced with Ser, Asp, Glu or Thr"
FT Misc-difference 110 /note= "optionally replaced with Met, Thr or Glu"
FT Misc-difference 114 /note= "optionally replaced with Asn"
FT Misc-difference 115 /note= "optionally replaced with Asn"
FT Misc-difference 126 /note= "optionally replaced with Asn"
FT Misc-difference 132 /note= "optionally replaced with Asn"
FT Misc-difference 134 /note= "optionally replaced with Thr"
FT Misc-difference 162 /note= "optionally replaced with Ala"
FT Misc-difference 166 /note= "optionally replaced with Asn"
FT

FT Misc-difference 169 /note= "optionally replaced with Ala"
 FT Misc-difference 171 /note= "optionally replaced with Asn"
 FT Misc-difference 172 /note= "optionally replaced with Asn"
 FT Misc-difference 179 /note= "optionally replaced with Thr"
 FT Misc-difference 183 /note= "optionally replaced with Lys"
 FT Misc-difference 194 /note= "optionally replaced with Asn"
 FT Misc-difference 196 /note= "optionally replaced with Thr"
 FT Misc-difference 209 /note= "optionally replaced with Thr"
 FT Misc-difference 225 /note= "optionally replaced with Thr"
 FT Misc-difference 237 /note= "optionally replaced with Arg"
 FT Misc-difference 270 /note= "optionally replaced with Glu"
 FT Misc-difference 270 /note= "optionally replaced with Gly"

PN WO200058465-A2.
 XX
 PD 05-OCT-2000.

PF 20-MAR-2000; 2000MO-US06417.
 XX
 XX 30-MAR-1999; 99US-0126839.
 PR 21-JUN-1999; 99US-0140077.
 PR 21-JUN-1999; 99US-0140156.
 PR 20-OCT-1999; 99US-0160566.
 PR 18-FEB-2000; 2000US-0183398.

XX (ELIL) LILLY & CO ELI.

PI Becker GW, Cohen FJ, Gonzalez-dewhitt PA, Hale JF, Micanovic R;
 PI Newton CM, Noblitt TW, Ratmachalam R, Tschang SR, Witcher DR;
 PI Wroblewski VJ;

XX WPI; 2000-656167/63.
 DR N-PSDB; AAA75999.

XX FAS ligand inhibitory Protein analogs useful for treating abnormal
 PT apoptosis related diseases e.g. acute lung injury, pulmonary fibrosis,
 PT chronic obstructive pulmonary disease ulcerative colitis or Crohn's
 PT disease -

PS Claim 1; Page 112-113; 114pp; English.

XX The present sequence represents a mature human FAS ligand inhibitory
 CC Protein (FLINT). FLINT is a homologue of tumour necrosis factor receptor
 CC proteins. FLINT inhibits the binding of FAS to FAS ligand. The mature
 CC FLINT protein is modified to produce analogues, which have greater
 CC potency, longer in vivo half-lives, decreased aggregation, decreased
 CC absorption onto surfaces, increased solubility and improved ease of
 CC formulation. The FLINT analogue is useful for treating a patient
 CC suffering from disease or condition relating to abnormal apoptosis such
 CC as acute lung injury, acute respiratory distress syndrome, pulmonary
 CC fibrosis, chronic obstructive pulmonary disease, ulcerative colitis, or
 CC Crohn's disease.

XX Sequence 271 AA;

Query Match 100.0%; Score 1491; DB 21; length 271;
 Best Local Similarity 100.0%; Pred. No. 8.5e-115;

Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VAETPTPMRDAEGERLVCACPPGTFVORPCRRDSTTTGPPCPPHRYTFMNYLERCR 60
 DB 1 VAETPTPMRDAEGERLVCACPPGTFVORPCRRDSTTTGPPCPPHRYTFMNYLERCR 60

QY 61 YCNVLGGEREEBARACHATHNRACRCRTGFFAHAGFLEHASCPGAGVIAPTPSQNTQ 120
 DB 61 YCNVLGGEREEBARACHATHNRACRCRTGFFAHAGFLEHASCPGAGVIAPTPSQNTQ 120
 QY 121 CQCPPEGTFSASSSSSSQCCPHRNCIALGLANVPSSSHDTICTSTGTPPLSTRVGAE 180
 DB 121 CQCPPEGTFSASSSSSSQCCPHRNCIALGLANVPSSSHDTICTSTGTPPLSTRVGAE 180
 QY 181 ECERAVIDFVAFODISIKRLQRLQALEAPEGMGPFRAGRALQKLRRLTEILGAOD 240
 DB 181 ECERAVIDFVAFODISIKRLQRLQALEAPEGMGPFRAGRALQKLRRLTEILGAOD 240
 QY 241 GALLVRLQALRVARMPEGLERSVREELPVH 271
 DB 241 GALLVRLQALRVARMPEGLERSVREELPVH 271

RESULT 3
 AAB19705
 ID AAB19705 standard; Protein; 271 AA.

XX AAB19705;

XX 05-FEB-2001 (first entry)

XX Human FAS ligand inhibitor protein FLINT.

XX FLINT; FAS ligand inhibitory protein; human; protease resistant;
 KW acute lung injury; acute respiratory distress syndrome;
 KW chronic obstructive pulmonary disease; pulmonary fibrosis;
 KW ulcerative colitis; therapy; organ transplantation.

XX Homo sapiens.

XX Key Location/Qualifiers
 FH Cleavage-site 218..219
 FT /note= "cleaved by trypsin-like proteases"

FT Misc-difference 34 /note= "optionally replaced by Arg, as given in
 FT Claims 10, 11, 13 and 14"

FT Misc-difference 36 /note= "optionally replaced by Thr, as given in
 FT Claims 10, 11, 13 and 14"

FT Misc-difference 132 /note= "optionally replaced by Asn, as given in
 FT Claim 12"

FT Misc-difference 194 /note= "optionally replaced by Asn, as given in
 FT Claims 11 and 14"

FT Misc-difference 196 /note= "optionally replaced by Thr, as given in
 FT Claims 11 and 14"

FT Misc-difference 214 /note= "optionally replaced by any naturally
 FT occurring amino acid"

FT Misc-difference 215 /note= "optionally replaced by any naturally
 FT occurring amino acid"

FT Misc-difference 216 /note= "optionally replaced by any naturally
 FT occurring amino acid, preferably Pro as
 FT given in Claims 9 and 15"

FT Misc-difference 217 /note= "optionally replaced by any naturally
 FT occurring amino acid, preferably Tyr as
 FT given in Claim 9"

FT Misc-difference 218 /note= "optionally replaced by any naturally
 FT occurring amino acid, preferably Glu, Glu,
 FT Ala, Gly, Ser, Val, Tyr or Asn as given in
 FT Claims, 9, 10, 11, 12, especially Glu as
 FT given in Claims 13, 14, 15, 35 and 36"

FT Misc-difference 219

FT /note= "optionally replaced by any naturally
 FT occurring amino acid"
 FT Misc-difference 220
 FT /note= "optionally replaced by any naturally
 FT occurring amino acid"
 FT Misc-difference 221
 FT /note= "optionally replaced by any naturally
 FT occurring amino acid"
 FT Misc-difference 222
 FT /note= "optionally replaced by any naturally
 FT occurring amino acid"
 XX WO200058466-A2.
 XX
 XX 05-OCT-2000.
 XX
 XX 20-MAR-2000; 2000WO-US06418.
 XX
 XX 30-MAR-1999; 99US-0126839.
 XX 21-JUN-1999; 99US-0140073.
 XX 04-AUG-1999; 99US-0147071.
 XX 20-OCT-1999; 99US-0160524.
 XX 21-OCT-1999; 99US-0160669.
 XX 20-DEC-1999; 99US-0172744.
 XX 26-JAN-2000; 2000US-0178184.
 XX
 XX (BLIL) LILLY & CO ELI.
 XX
 XX Micanovic R, Rathnachalam R, Witcher DR;
 XX
 XX WPI; 2000-664925/64.
 XX N-PSDB; AAA88730.
 XX
 XX Novel protease resistant FAS ligand inhibitory protein analogues
 PT resistant to in vivo or in vitro proteolysis at amino acid position 218
 PT of the mature protein, useful for treating autoimmune diseases
 XX
 XX Claim 1; Page 94-95; 100pp; English.
 XX
 XX The present sequence is that of human FAS ligand inhibitory protein
 CC FLINT mature protein. FLINT is a tumour necrosis factor receptor
 CC homologue that binds FAS ligand, preventing its interaction with
 CC FAS. This interaction is implicated in runaway apoptosis and
 CC inflammatory disease. FLINT also binds to LIGHT, a membrane-bound
 CC ligand, which may play a role in immune modulation and apoptosis.
 CC The invention relates to novel FLINT analogues (see also AAB19706-09)
 CC that are resistant to proteolysis by trypsin-like proteases between
 CC positions 218 and 219 of the FLINT mature protein sequence. The
 CC analogues have amino acid substitutions in the region comprising
 CC amino acids 214-222, and may contain additional substitutions at
 CC residues 34, 36, 132, 194 and/or 196. Nucleic acids, vectors and
 CC transformed host cells for recombinant production of the analogues
 CC are claimed. FLINT cDNA (see AAA88730) is used as a template for
 CC introducing the required point mutations. The protease resistant
 CC FLINT analogues are used to prevent or treat acute lung injury,
 CC acute respiratory stress syndrome, ulcerative colitis, chronic
 CC obstructive pulmonary disease, pulmonary fibrosis, to inhibit T
 CC lymphocyte activation, and to facilitate organ preservation for
 CC transplantation (claimed).
 XX
 XX Sequence 271 AA;
 SQ
 Query Match 100.0%; Score 1491; DB 21; Length 271;
 Best Local Similarity 100.0%; Pred. No. 8.5e-115;
 Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VAETPTTWRDAETGERLVCACQCPGTFVQPCRRDSPTTCGCPPRHYTFQWNYLERCR 60
 DB 1 VAETPTTWRDAETGERLVCACQCPGTFVQPCRRDSPTTCGCPPRHYTFQWNYLERCR 60
 QY 61 YCNVLCGEREEARACHATHNRCRCRTGTFPAHAGFCLHASCPPGAGVIAPGTPSQNTQ 120
 DB 61 YCNVLCGEREEARACHATHNRCRCRTGTFPAHAGFCLHASCPPGAGVIAPGTPSQNTQ 120

QY 121 CQPCPGTFSASSSSSECOCPHRNCTALGLALNVPGSSSHDTLCTCTGFPILSTRVPGAE 180
 DB 121 CQPCPGTFSASSSSSECOCPHRNCTALGLALNVPGSSSHDTLCTCTGFPILSTRVPGAE 180
 QY 181 ECERAVIDFVAFODISIKRLQRLQALEAPEGWGPTFRAGRAALQKLRRRLTELLGAQD 240
 DB 181 ECERAVIDFVAFODISIKRLQRLQALEAPEGWGPTFRAGRAALQKLRRRLTELLGAQD 240
 QY 241 GALLVRLQALRVARMPLGLERSVRERFLPVH 271
 DB 241 GALLVRLQALRVARMPLGLERSVRERFLPVH 271
 RESULT 4
 AAY97247
 ID AAY97247 standard; Protein; 271 AA.
 XX
 AC AAY97247;
 XX
 DT 19-DEC-2000 (first entry)
 XX
 DE M68 TNF receptor related protein (mature protein).
 XX
 KW M68: tumour necrosis factor; TNF; programmed cell death; apoptosis;
 KW receptor; immune response; cell differentiation; ligand; cancer;
 KW bone disease; systemic lupus erythematosus; Hashimoto's thyroiditis;
 KW Grave's disease; idiopathic myxedema; autoimmune diabetes;
 KW thrombotic thrombocytopenic purpura; multiple sclerosis;
 KW liver diseases; autoimmune gastritis; ulcerative colitis;
 KW glomerulonephritis; pulmonary fibrosis; heart failure;
 KW atherosclerosis; aplastic anaemia; myelodysplastic syndromes;
 KW osteoporosis; Alzheimers disease; Parkinsons disease; stroke;
 KW myocardial infarction; human.
 XX
 OS Homo sapiens.
 XX
 PN WO200046247-A1.
 XX
 PD 10-AUG-2000.
 XX
 PF 04-FEB-2000; 2000WO-US03037.
 XX
 PR 05-FEB-1999; 99US-0118902.
 PR 20-DEC-1999; 99US-0172754.
 XX
 PA (MERI) MERCK & CO INC.
 XX
 PI Bai C;
 XX
 WIPI; 2000-506066/45.
 XX
 PT Isolated human M68 nucleic acids and proteins which are part of the
 PT tumor necrosis factor receptor (TNFR) family, useful for identifying
 PT modulators that may be used to treat various diseases e.g. cancer,
 PT osteoporosis, Alzheimer's disease
 XX
 PS Claim 1; Page 76; 80pp; English.
 XX
 CC The M68 protein is a member of a family of proteins which have
 CC roles in immune responses, cell death, cell proliferation and
 CC stimulation of cell differentiation. M68 lacks a transmembrane domain
 CC and is a secreted factor suggesting that it functions as a natural
 CC inhibitor for its ligand. The altered expression pattern of M68 in a
 CC multitude of tissues suggests that M68 may play a role in cancer by
 CC binding to its ligand and blocking apoptotic cell death induced by
 CC such a ligand. This anti-apoptotic role of M68 suggests that
 CC modulators of M68 will be useful in treatment of apoptosis-related
 CC diseases such as various forms of cancer and various bone disorders.
 CC M68 nucleic acids and proteins are therefore useful for treating
 CC conditions involving atypical apoptosis and for identifying
 CC modulators of M68. Modulators of M68 are useful for treatment of
 CC cancer and other diseases associated with abnormal levels of

CC apoptosis including systemic lupus erythematosus, Hashimoto's
 CC thyroiditis, Grave's disease, idiopathic myxedema, autoimmune
 CC diabetes, thrombotic thrombocytopenic purpura, multiple sclerosis,
 CC liver diseases, autoimmune gastritis, ulcerative colitis,
 CC glomerulonephritis, pulmonary fibrosis, heart failure,
 CC atherosclerosis, aplastic anaemia, myelodysplastic syndromes,
 CC osteoporosis, Alzheimer's disease, Parkinson's disease, stroke, and
 CC myocardial infarction.
 XX
 SO Sequence 271 AA:
 Query Match 100.0%; Score 1491; DB 21; Length 271;
 Best Local Similarity 100.0%; Pred. No. 8.5e-115;
 Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VAEPTPYPMWDAETGERLVCAQCPPTGVQPCRRDSPPTTCGCPRRHYTOFNNYLERCR 60
 DB 1 VAETPTYPWMDAETGERLVCAQCPPTGVQPCRRDSPPTTCGCPRRHYTOFNNYLERCR 60
 QY 61 YCNVLGGEREEERACHATNRAACRCRTGFFAHAGFCLHASCPPGAGYIAPGPSQNTQ 120
 DB 61 YCNVLGGEREEERACHATNRAACRCRTGFFAHAGFCLHASCPPGAGYIAPGPSQNTQ 120
 QY 121 CQCPPTGTFSSASSSSSEOCQPHNCTALGLALNVGSSSHDTLCTSCGFPPLSTRVPGAE 180
 DB 121 CQCPPTGTFSSASSSSSEOCQPHNCTALGLALNVGSSSHDTLCTSCGFPPLSTRVPGAE 180
 QY 181 ECRRAVIDFVAFODISIKRLQRLQALEAPBEGMPTPRAGRAALQKLRRRLTELLGAOD 240
 DB 181 ECRRAVIDFVAFODISIKRLQRLQALEAPBEGMPTPRAGRAALQKLRRRLTELLGAOD 240
 QY 241 GALLVRLQALRVARNMPGLERSVREERFLPVH 271
 DB 241 GALLVRLQALRVARNMPGLERSVREERFLPVH 271
 RESULT 5
 AAY96598
 ID AAY96598 standard; Protein; 271 AA.
 XX
 AC AAY96598;
 DT 26-SEP-2000 (first entry)
 XX
 DE Human mature FLINT.
 XX
 KM FLINT; osteoprotegerin 3, OPG3; tumour necrosis factor receptor; TNFR,
 KM FasL; LIGHT; apoptosis; pro-inflammatory; hepatotropic; vasotrophic;
 KM anti-diabetic; anti-anaemic; neuroprotective; anti-ulcer; cycostatic;
 KM anti-inflammatory; antibacterial; immunosuppressive.
 XX
 OS Homo sapiens.
 XX
 PN WO200037094-A2.
 XX
 PD 29-JUN-2000.
 XX
 PF 21-DEC-1999; 99WO-US30734.
 XX
 PR 22-DEC-1998; 98US-0113407.
 PR 30-MAR-1999; 99WO-US06797.
 PR 20-OCT-1999; 99US-0172239.
 XX
 PA (ELIL) LILLY & CO ELI.
 XX
 PI Cohen FU, Posada JA, Wierda D;
 XX
 DR WPI; 2000-475441/41.
 DR N-PSDB; AAA51077.
 XX
 PT Use of mature FLINT for treating e.g. acute respiratory distress
 PT syndrome, ulcerative colitis or ischemic injury during organ
 PT transplantation

XX
 PS Example 8; Fig 3; 125pp; English.
 XX
 CC Human FLINT (also known as osteoprotegerin 3) is a new tumour necrosis
 CC factor receptor (TNFR) superfamily member, which binds FasL and LIGHT and
 CC prevents FasL-Fas interaction. Mature FLINT (mFLINT) inhibits FasL-Fas
 CC mediated apoptotic and pro-inflammatory activity. mFLINT is useful for
 CC treating acute respiratory distress syndrome, treating or inhibiting
 CC ulcerative colitis, inhibiting ischemic injury during organ
 CC transplantation or for organ preservation during transplantation. mFLINT
 CC can also be used to treat acute liver failure, inflammation of the liver,
 CC abnormal (hepatocyte) apoptosis, sepsis, disorders associated with
 CC inflammation, hepatitis, ischemia, hypercoagulation or reperfusion,
 CC damage to a cardiac myocyte resulting from abnormal myocardial ischemia,
 CC Type I diabetes, cancer, damage to an innocent bystander tissue induced
 CC by a chemotherapeutic or therapeutic irradiation, aplastic anaemias,
 CC myelodysplastic syndromes and pancytopenic conditions.
 XX
 SO Sequence 271 AA:
 Query Match 100.0%; Score 1491; DB 21; Length 271;
 Best Local Similarity 100.0%; Pred. No. 8.5e-115;
 Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VAEPTPYPMWDAETGERLVCAQCPPTGVQPCRRDSPPTTCGCPRRHYTOFNNYLERCR 60
 DB 1 VAETPTYPWMDAETGERLVCAQCPPTGVQPCRRDSPPTTCGCPRRHYTOFNNYLERCR 60
 QY 61 YCNVLGGEREEERACHATNRAACRCRTGFFAHAGFCLHASCPPGAGYIAPGPSQNTQ 120
 DB 61 YCNVLGGEREEERACHATNRAACRCRTGFFAHAGFCLHASCPPGAGYIAPGPSQNTQ 120
 QY 121 CQCPPTGTFSSASSSSSEOCQPHNCTALGLALNVGSSSHDTLCTSCGFPPLSTRVPGAE 180
 DB 121 CQCPPTGTFSSASSSSSEOCQPHNCTALGLALNVGSSSHDTLCTSCGFPPLSTRVPGAE 180
 QY 181 ECRRAVIDFVAFODISIKRLQRLQALEAPBEGMPTPRAGRAALQKLRRRLTELLGAOD 240
 DB 181 ECRRAVIDFVAFODISIKRLQRLQALEAPBEGMPTPRAGRAALQKLRRRLTELLGAOD 240
 QY 241 GALLVRLQALRVARNMPGLERSVREERFLPVH 271
 DB 241 GALLVRLQALRVARNMPGLERSVREERFLPVH 271
 RESULT 6
 AAE03567
 ID AAE03567 standard; Protein; 271 AA.
 XX
 AC AAE03567;
 DT 04-AUG-2001 (first entry)
 XX
 DE Human mature fas ligand inhibitory protein (FLINT).
 XX
 KM Human; fas ligand inhibitory protein; FLINT; acute lung injury; ALI;
 KM TNFR; tumour necrosis factor receptor protein; ulcerative colitis; ARDS;
 KM acute respiratory distress syndrome; pulmonary fibrosis; PF; therapy;
 KM chronic obstructive pulmonary disease; COPD; acute lung injury; goitre;
 KM rheumatoid arthritis; fibroproliferative lung disease; ischaemia; sepsis;
 KM fibrotic lung disease; human immunodeficiency virus; HIV; osteoporosis;
 KM chronic renal failure; graft-ve-host disease; cutaneous inflammation;
 KM vascular leak syndrome; Helicobacter pylori infection; atherosclerosis;
 KM insulin dependent diabetes mellitus (IDDM); inflammatory bowel disease;
 KM Crohn's disease; pancreatitis; cancer; autoimmune disease; psoriasis;
 KM Down's syndrome; multiple sclerosis; cycostatic; neurotropic;
 KM neuroprotective; vasotrophic.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 144
 FT /note= "N-linked glycosylation site"

FT Modified-site 174 /note= "O-linked glycosylation site"
 FT FT 216
 FT Modified-site /note= "O-linked glycosylation site"
 FT FT 218..219
 FT Cleavage-site /note= "Proteolytic cleavage"

XX WO200142463-A1.

XX PN

XX PD

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Db 241 GALLVRLQLQALRVARMPGLERSVRERFLPVH 271

RESULT 7

AAB68044

ID AAB68044 standard; Protein; 271 AA.

XX AAB68044;

XX AAB68044;

XX 29-JUN-2001 (first entry)

XX Amino acid sequence of a human mature FLINT polypeptide.

XX FLINT; FAS ligand inhibitory protein; divalent metal cation; Fas;

XX Fas ligand; acute liver failure; cerebral ischemia; apoptosis.

XX Homo sapiens.

XX WO200118055-A1.

XX 15-MAR-2001.

XX 31-AUG-2000; 2000WO-US20807.

XX 10-SEP-1999; 99US-0153339.

XX (ELIL) LILLY & CO ELI.

XX Atkinson PR, Tian Y, Witcher DR;

XX WPI; 2001-273382/28.

XX Compositions comprising a divalent metal cation and a FAS Ligand

XX Inhibitory Protein (FLINT), for reducing or inducing aggregation of

XX FLINT and for treating diseases involving FasL/Fas and/or

XX LIGHT/LT-beta-R receptor interactions

XX Example 1; Page 39-40; 44pp; English.

XX The present sequence represents a mature FLINT (FAS Ligand Inhibitory

XX Protein) polypeptide. The specification describes a composition

XX comprising a divalent metal cation and FLINT protein. The composition

XX is used either for reducing, reversing or eliminating aggregation and

XX precipitation of FLINT or for inducing oligomerisation or aggregation

XX of FLINT molecules. They can be used for purifying FLINT and/or

XX maintaining FLINT in solution. The compositions are used to treat

XX and/or prevent disorders associated with the binding of Fas to FasL

XX and/or LIGHT to the LtbetaR and/or TR2/HVEM receptors. Uses include the

XX treatment of acute liver failure and cerebral ischemia and the prevention

XX of apoptosis.

XX SQ Sequence 271 AA;

XX Query Match 100.0%; Score 1491; DB 22; Length 271;

XX Best Local Similarity 100.0%; Pred. No. 8.5e-115;

XX Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX QY 1 VAETPTYPWRDAETGERLVCAQCPGTFVQPCRRDSPTTCGCPPRHYTOFWNYLERCR 60

XX Db 1 VAETPTYPWRDAETGERLVCAQCPGTFVQPCRRDSPTTCGCPPRHYTOFWNYLERCR 60

XX QY 61 YCNVLCGEREEERACHATHNRACRGTGFFAHAGFCLFHASCPGAGVIAPGTPSQNTQ 120

XX Db 61 YCNVLCGEREEERACHATHNRACRGTGFFAHAGFCLFHASCPGAGVIAPGTPSQNTQ 120

XX QY 121 CQCPPGTFSASSSSSQCPHRNCTALGLALNVPGSSSHDTLCTSGTGFPLSTRVPGAE 180

XX Db 121 CQCPPGTFSASSSSSQCPHRNCTALGLALNVPGSSSHDTLCTSGTGFPLSTRVPGAE 180

XX QY 181 ECERAVIDFVAFQDISIKRLQRLLOALEAPEGWGTPPRAGRAALQLKLRRLTELLGAQD 240

XX Db 181 ECERAVIDFVAFQDISIKRLQRLLOALEAPEGWGTPPRAGRAALQLKLRRLTELLGAQD 240

XX QY 241 GALLVRLQLQALRVARMPGLERSVRERFLPVH 271

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QY 241 GALLVRLQLALRVARMPGLERSVREERFLPVH 271
 DB 241 GALLVRLQLALRVARMPGLERSVREERFLPVH 271

RESULT 8

AAB68047 standard; Protein; 271 AA.

AC AAB68047;

DT 29-JUN-2001 (first entry)

DE Amino acid sequence of a human mature FLINT polypeptide.

KM FLINT; FAS ligand inhibitory protein; divalent metal cation; Fas;
 KW Fas ligand; acute liver failure; cerebral ischemia; apoptosis.

OS Homo sapiens.

PN WO200118041-A2.

PD 15-MAR-2001.

PF 31-AUG-2000; 2000WO-US20805.

PR 10-SEP-1999; 99US-0153445.

PA (ELIL) LILLY & CO ELI.

PI Atkinson PR, Tian Y, Witcher DR;

DR WPI; 2001-273381/28.

PT Compositions comprising a divalent metal cation and a FAS ligand
 PT Inhibitory Protein (FLINT), for reducing or inducing aggregation of
 PT FLINT and for treating diseases involving FasL/Fas and/or
 PT LIGHT/Lt-beta-R receptor interactions -

PS Disclosure; Page 30-31; 33pp; English.

XX The present sequence represents a human mature FLINT (FAS ligand
 CC Inhibitory Protein) polypeptide. The specification describes a
 CC composition comprising a divalent metal cation and FLINT protein. The
 CC composition is used either for reducing, reversing or eliminating
 CC aggregation and precipitation of FLINT or for inducing oligomerisation
 CC or aggregation of FLINT molecules. They can be used for purifying FLINT
 CC and/or maintaining FLINT in solution. The compositions are used to treat
 CC and/or prevent disorders associated with the binding of Fas to FasL
 CC and/or LIGHT to the lmbeta-R and/or TR2/HVEM receptors. Uses include the
 CC treatment of acute liver failure and cerebral ischemia and the prevention
 CC of apoptosis.

SQ Sequence 271 AA;

Query Match 100.0%; Score 1491; DB 22; Length 271;

Best Local Similarity 100.0%; Pred. No. 8.5e-115; Mismatches 0; Indels 0; Gaps 0;

DB 1 VAEPTPYPMRDATGRLVCAQCPPTGVQRCRRDPTTCGCPRRHYTOFNNYLERCR 60

QY 1 VAEPTPYPMRDATGRLVCAQCPPTGVQRCRRDPTTCGCPRRHYTOFNNYLERCR 60

DB 61 YCNVLGGEREEERACHATNRAACRGTGFPAHAGFCLHASCPPGAGVIAETPSQNTQ 120

QY 61 YCNVLGGEREEERACHATNRAACRGTGFPAHAGFCLHASCPPGAGVIAETPSQNTQ 120

DB 121 CQCPPTGTSASSSSSEQCPHNRCTALGLALNVPGSSSHDTLCTSGTFPLSTRVPGE 180

QY 121 CQCPPTGTSASSSSSEQCPHNRCTALGLALNVPGSSSHDTLCTSGTFPLSTRVPGE 180

DB 121 CQCPPTGTSASSSSSEQCPHNRCTALGLALNVPGSSSHDTLCTSGTFPLSTRVPGE 180

QY 181 ECRRAVIDVAFODISIKRLQRLQLEAPEGWGPTRAGRALQLKLRRLTELLGAOD 240

DB 181 ECRRAVIDVAFODISIKRLQRLQLEAPEGWGPTRAGRALQLKLRRLTELLGAOD 240
 QY 241 GALLVRLQLALRVARMPGLERSVREERFLPVH 271
 DB 241 GALLVRLQLALRVARMPGLERSVREERFLPVH 271

RESULT 9

AAB74465 standard; protein; 271 AA.

AC AAB74465;

DT 30-MAY-2001 (first entry)

DE Human FLINT mature protein.

KM Human; FLINT; FAS ligand inhibitory protein; analogue; apoptosis;
 KW inflammatory disease.

OS Homo sapiens.

PN WO200118202-A2.

PD 15-MAR-2001.

PF 31-AUG-2000; 2000WO-US20806.

PR 10-SEP-1999; 99US-0153433.

PA (ELIL) LILLY & CO ELI.

PI Atkinson PR, Tian Y, Witcher DR;

DR WPI; 2001-257796/26.

PT Compositions useful for reducing/inducing aggregation of a FLINT analog
 PT comprise a divalent metal cation and a protease-resistant FAS ligand
 PT Inhibitory Protein (FLINT) analog -

PS Claim 4; Page 41-42; 44pp; English.

XX The present invention describes a composition comprising a divalent metal
 CC cation associated with a protease resistant Fas ligand inhibitory protein
 CC (FLINT) analogue. The composition is useful in the treatment of diseases
 CC associated with Fas binding to its ligand, such as acute liver failure,
 CC inflammatory diseases, cerebral ischaemia and apoptosis. The present
 CC sequence is the mature FLINT protein.

SQ Sequence 271 AA;

Query Match 100.0%; Score 1491; DB 22; Length 271;

Best Local Similarity 100.0%; Pred. No. 8.5e-115; Mismatches 0; Indels 0; Gaps 0;

DB 1 VAEPTPYPMRDATGRLVCAQCPPTGVQRCRRDPTTCGCPRRHYTOFNNYLERCR 60

QY 1 VAEPTPYPMRDATGRLVCAQCPPTGVQRCRRDPTTCGCPRRHYTOFNNYLERCR 60

DB 61 YCNVLGGEREEERACHATNRAACRGTGFPAHAGFCLHASCPPGAGVIAETPSQNTQ 120

QY 61 YCNVLGGEREEERACHATNRAACRGTGFPAHAGFCLHASCPPGAGVIAETPSQNTQ 120

DB 121 CQCPPTGTSASSSSSEQCPHNRCTALGLALNVPGSSSHDTLCTSGTFPLSTRVPGE 180

QY 121 CQCPPTGTSASSSSSEQCPHNRCTALGLALNVPGSSSHDTLCTSGTFPLSTRVPGE 180

DB 181 ECRRAVIDVAFODISIKRLQRLQLEAPEGWGPTRAGRALQLKLRRLTELLGAOD 240

QY 181 ECRRAVIDVAFODISIKRLQRLQLEAPEGWGPTRAGRALQLKLRRLTELLGAOD 240

DB 241 GALLVRLQLALRVARMPGLERSVREERFLPVH 271

Db 241 GALLVRLQALRVARMPGLSVRRFLPVH 271

RESULT 10
AAE14578
ID AAE14578 standard; Protein; 271 AA.

AC AAE14578;

XX 01-JUL-2002 (first entry)

DT Human mature FLINT protein.

XX FLINT; FAS ligand inhibitory protein; pulmonary; lung; apoptosis;
KW organ failure; liver; kidney; pancreas; inflammatory disease;
KW neutrophil; sepsis; acute respiratory distress syndrome;
KW acute lung injury; systemic inflammatory response syndrome; SIRS;
KW multiple organ dysfunction; MODS; human.

XX Homo sapiens.

XX WO200209668-A2.

XX 07-FEB-2002.

XX 20-JUL-2001; 2001WO-US211105.

XX 02-AUG-2000; 2000US-222476P.

XX (ELIL) LILLY & CO ELI.

XX Micanovic R, Witcher DR;

XX WPI; 2002-206149/26.

XX N-PSDB; AAD27868.

XX Administering FLINT (FAS ligand inhibitory protein) or FLINT analog,
PT useful for treating e.g. sepsis or respiratory distress syndrome,
PT involves pulmonary administration of a therapeutic amount of the FLINT
PT or FLINT analog -

XX Disclosure; Page 29-30; 35pp; English.

XX The invention relates to a new method of administering FLINT
XX (FAS ligand inhibitory protein) or FLINT analog that involves pulmonary
XX administration of a therapeutic amount of the FLINT or FLINT analog.
XX The method enables systemic absorption of FLINT through lungs and
XX significantly reduces or eliminates the need for administering FLINT by
XX injection or other routes of administration. The method is useful in
XX treating disorders related to enhanced apoptosis (e.g. organ failure
XX in liver, kidneys and pancreas) and inflammatory diseases associated with
XX neutrophil activation (e.g. sepsis, acute respiratory distress syndrome,
XX acute lung injury, systemic inflammatory response syndrome (SIRS) and
XX multiple organ dysfunction (MODS)). The method minimises the pain
XX and discomfort of injection methods. The present sequence is human
XX mature FLINT protein.

XX Sequence 271 AA;

SQ Query Match 100.0%; Score 1491; DB 23; Length 271;
Best Local Similarity 100.0%; Pred. No. 8.5e-115;
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VAETPTYPWRDAETGERLVCAQCPGTFVORPCRDSDPTTCGCPPRHYTQFWNYLERCR 60

Db 1 VAETPTYPWRDAETGERLVCAQCPGTFVORPCRDSDPTTCGCPPRHYTQFWNYLERCR 60

Qy 61 YCNVLCGEREEARACHATHNACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120

Db 61 YCNVLCGEREEARACHATHNACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120

Qy 121 CQPCPPGTFSSSSSEQPHRNCALGLALNVPGSSSHDTLCTSGTGFPLSTRVPGAE 180

Db 121 CQPCPPGTFSSSSSEQPHRNCALGLALNVPGSSSHDTLCTSGTGFPLSTRVPGAE 180

Qy 181 ECERAVIDFVAFQDISIKLQRLQALEAPEGPGTPPRAGRAALQKLRRRLTELLGAQD 240

Db 181 ECERAVIDFVAFQDISIKLQRLQALEAPEGPGTPPRAGRAALQKLRRRLTELLGAQD 240

Qy 241 GALLVRLQALRVARMPGLSVRRFLPVH 271

Db 241 GALLVRLQALRVARMPGLSVRRFLPVH 271

RESULT 11

AAW66102

ID AAW66102 standard; Protein; 300 AA.

AC AAW66102;

XX 02-DEC-1998 (first entry)

DE Amino acid sequence of tumour necrosis related receptor (TR4).

XX Human; tumour necrosis related receptor; TR4; agonist; antagonist;
KW inhibition; chronic; acute; inflammation; arthritis; septicaemia;
KW autoimmune disease; transplant rejection; stroke; cancer;
KW Alzheimer's disease.

XX Homo sapiens.

XX EP861850-A1.

XX 02-SEP-1998.

XX 20-JAN-1998; 98EP-0300382.

XX 04-FEB-1997; 97US-0794796.

XX (SMIK) SMITHKLINE BEECHAM CORP.

XX Emery J, Tan KB, Truneh A, Young PR;

XX WPI; 1998-508248/44.

XX N-PSDB; AAV07654.

XX New DNA encoding tumour necrosis related receptor - used to treat
XX and prevent e.g. inflammation, arthritis, septicaemia, autoimmune
XX diseases, transplant rejection, infection, stroke, ischaemia, ARDS,
XX restenosis, AIDS, bone disorders and cancer

XX Claim 1; Fig 1; 21pp; English.

XX This is the amino acid sequence of the human tumour necrosis related
XX receptor (TR4), used in the method of the invention. The TR4 protein
XX or its agonist can be used to treat a subject in need of enhanced
XX TR4 polypeptide activity. The antagonist is used to inhibit TR4
XX polypeptide activity. The active agents can be used for the
XX treatment and prevention of diseases such as chronic and acute
XX inflammation, arthritis, septicaemia, autoimmune diseases, transplant
XX rejection, stroke, cancer, Alzheimer's disease.

XX Sequence 300 AA;

SQ Query Match 100.0%; Score 1491; DB 19; Length 300;
Best Local Similarity 100.0%; Pred. No. 9.6e-115;
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VAETPTYPWRDAETGERLVCAQCPGTFVORPCRDSDPTTCGCPPRHYTQFWNYLERCR 60

Db 30 VAETPTYPWRDAETGERLVCAQCPGTFVORPCRDSDPTTCGCPPRHYTQFWNYLERCR 89

Qy 61 YCNVLCGEREEARACHATHNACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120

Db 90 YCNVLCGEREEARACHATHNACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 149

QY 121 CQPCPGTFSASSSSQCPHNRCTALGLALNPGSSHDLTCTSGTGFPLSTRVPGAE 180
 Db 150 CQPCPGTFSASSSSQCPHNRCTALGLALNPGSSHDLTCTSGTGFPLSTRVPGAE 209
 QY 181 ECERAVIDFVAFODISIKRLQRLQLALEAPEGWPPTPRAGRAALQLKLRRLTELLGAQD 240
 Db 210 ECERAVIDFVAFODISIKRLQRLQLALEAPEGWPPTPRAGRAALQLKLRRLTELLGAQD 269
 QY 241 GALLVRLQLARVARMGELERSYVERFLPVH 271
 Db 270 GALLVRLQLARVARMGELERSYVERFLPVH 300
 RESULT 12
 AAM63622
 ID AAM63622 standard; Protein; 300 AA.
 AC AAM63622;
 XX
 DT 26-OCT-1998 (first entry)
 XX
 DE Human tumour necrosis factor receptor-6 alpha protein.
 XX
 KW Human tumour necrosis factor receptor-6 alpha; TNFR-6 alpha; TNFR-6 beta;
 KM endocheial cells; keratinocytes; normal prostate; apoptosis;
 KM prostate tumour tissue.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..30
 FT Protein 31..300
 FT /note= "TNFR-6 alpha"
 FT Region 31..282
 FT /note= "Soluble extracellular domain"
 XX
 PN MO9830694-A2.
 XX
 PD 16-JUL-1998.
 XX
 PF 13-JAN-1998; 98MO-US00153.
 XX
 PR 14-JAN-1997; 97US-0035496.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Ebner R, Feng P, Gentz RL, Ni J, Ruben SM, Yu G;
 XX WPI: 1998-399142/34.
 DR N-PSDB; AAV39085.
 XX
 PT Human tumour necrosis factor receptors 6-alpha and 6-beta - used in
 PT the diagnosis of immune system-related disorder(s)
 XX
 PS Claim 20; Fig 1; 91pp; English.
 CC The present sequence represents the human tumour necrosis factor
 CC receptor-6 alpha (TNFR-6 alpha) protein. The invention also provides
 CC for the TNFR-6 beta protein (AAM63623). TNFR-6 alpha and TNFR-6 beta
 CC are members of the tumour necrosis factor receptor (TNFR) family. TNFRs
 CC are expressed in endothelial cells, keratinocytes, normal prostate and
 CC prostate tumour tissue. For a number of disorders of these cells,
 CC particularly of the immune system, substantially altered (whether
 CC increased or decreased) levels of TNFR-6 alpha and/or TNFR-6 beta gene
 CC expression can be detected, therefore the TNFR-6 alpha and TNFR-6 beta
 CC polypeptides, nucleic acids and antibodies are claimed to be useful in
 CC the diagnosis of such disorders. Mutations of the TNFR-6 alpha and
 CC TNFR-6 beta genes can also be detected. The TNFR polypeptides are
 CC also claimed to be useful for identifying ligands which may be useful
 CC in the treatment of apoptosis related disorders.
 CC
 XX Sequence 300 AA;
 XX

Query Match 100.0%; Score 1491; DB 19; Length 300;
 Best Local Similarity 100.0%; Pred. No. 9.6e-115;
 Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VAEPTPYMWDAGTEGRLVCAQCPGTFVORPCRBDSPITCGPCPRHYTOFMNYLERCR 60
 Db 30 VAEPTPYMWDAGTEGRLVCAQCPGTFVORPCRBDSPITCGPCPRHYTOFMNYLERCR 89
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 QY 121 CQPCPGTFSASSSSQCPHNRCTALGLALNPGSSHDLTCTSGTGFPLSTRVPGAE 180
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 QY 241 GALLVRLQLARVARMGELERSYVERFLPVH 271
 Db 270 GALLVRLQLARVARMGELERSYVERFLPVH 300
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 AAY03099
 ID AAY03099 standard; Protein; 300 AA.
 AC AAY03099;
 XX
 DT 09-DEC-1999 (first entry)
 XX
 DE Human lung TNF-receptor protein.
 XX
 KW Tumour necrosis factor; TNF; TNF receptor; human; lung; gene therapy;
 KM detection; immunosassay; diagnosis; disease; immune system; tumour;
 KM osteogenic system; cardiovascular system; central nervous system; asthma;
 KM peripheral nervous systems; transplant incompatibility; antitumor;
 KM rheumatoid arthritis; antiasthmatic; antiarthritic.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 134..1036
 FT /*tag= a
 FT /product= "TNF-receptor"
 XX
 PN DE19809978-A1.
 XX
 PD 16-SEP-1999.
 XX
 PF 09-MAR-1998; 98DE-1009978.
 XX
 PR 09-MAR-1998; 98DE-1009978.
 XX
 PA (BADT) BASF AG.
 XX
 PI Kroeger B;
 XX WPI: 1999-519473/44.
 DR N-PSDB; AAZ09998.
 XX
 PT New soluble member of tumor necrosis factor receptor family, useful for
 PT identification specific modulators and for treating disease e.g. tumors
 XX
 PS Claim 1; Page 8-9; 10pp; German.
 CC This invention describes a novel tumour necrosis factor (TNF) receptor
 CC (I) isolated from human lung tissue. (I) is used; (i) to raise specific
 CC antibodies (Ab); (ii) to screen for specific (ant)agonists or ligands

CC (A), potential therapeutic agents; and (iii) therapeutically (optionally
 CC expressed from a gene therapy vector) in conditions associated with a
 CC deficit of (I). Ab are used: (a) for qualitative or quantitative
 CC detection of (I) in standard immunoassays (for diagnosis of disease, or
 CC susceptibility, or for monitoring); and (b) as therapeutic inhibitors in
 CC cases where (I) is overexpressed. Nucleic acid (II) that encodes (I) is
 CC used: (A) for recombinant production of (I); (B) also its oligonucleotide
 CC fragments, in standard hybridization and/or amplification assays; (C) as
 CC source of antisense molecules or ribozymes; and (D) to produce transgenic
 CC animals (for studying (patho)physiology of (I)). Diseases possibly
 CC associated with under- or over-expression of (I) are those of the immune,
 CC osteogenic, cardiovascular and central or peripheral nervous systems,
 CC tumors, transplant incompatibility, asthma and rheumatoid arthritis. The
 CC products of the invention have antitumor, antiasthmatic and
 CC antiarthritic activity. This sequence represents the TNF-receptor of the
 CC invention.

XX SQ Sequence 300 AA;

Query Match 100.0%; Score 1491; DB 20; Length 300;
 Best Local Similarity 100.0%; Pred. No. 9.6e-115;
 Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VAETPTYPWRDAETGERLVCAQCPGGTFVQPCRRDSPTTCGCPPRHYTFQWNYLERCR 60
 Db 30 VAETPTYPWRDAETGERLVCAQCPGGTFVQPCRRDSPTTCGCPPRHYTFQWNYLERCR 89
 Qy 61 YCNVLCGEREEERACHATHNACRCRTGFFAHAGFCLEHASCPGAGVIAPGTPSQNTQ 120
 Db 90 YCNVLCGEREEERACHATHNACRCRTGFFAHAGFCLEHASCPGAGVIAPGTPSQNTQ 149
 Qy 121 CQPCPPGTFSSSSSQCPHRCNTALGLALNVPGSSSHDTLTCTSGTGPLSTRVPGAE 180
 Db 150 CQPCPPGTFSSSSSQCPHRCNTALGLALNVPGSSSHDTLTCTSGTGPLSTRVPGAE 209
 Qy 181 ECERAVIDFVAFQDISIKRLQLQLEAPEGNGTTPRAGRAALQLKRLRLTELLGAQD 240
 Db 210 ECERAVIDFVAFQDISIKRLQLQLEAPEGNGTTPRAGRAALQLKRLRLTELLGAQD 269

RESULT 14

AAV42182
 ID AAV42182 standard; Protein; 300 AA.

XX AC AAY42182;

XX 17-DEC-1999 (first entry)

XX Human FLINT #1 protein sequence.

XX Human; FLINT; mFLINT; OPG3; tumour necrosis factor receptor; FasL;
 KW apoptosis; inflammation; cancer; diabetes; acute liver failure;
 KW sepsis; hepatitis; ischaemia-associated injury; hypercoagulation;
 KW reperfusion-associated injury; aplastic anaemia; differentiation;
 KW growth; myelodysplastic syndrome; pancytopenic condition;
 KW myocardial ischaemia.

OS Homo sapiens.

XX WO9950413-A2.

XX 07-OCT-1999.

XX 30-MAR-1999; 99WO-US06797.

XX 30-MAR-1998; 98US-0079856.

XX 20-MAY-1998; 98US-0086074.

XX 09-SEP-1998; 98US-0099643.

XX 17-DEC-1998; 98US-0112577.

PR 18-DEC-1998; 98US-0112703.
 PR 18-DEC-1998; 98US-0112933.
 PR 22-DEC-1998; 98US-0113407.
 XX (ELIL) LILLY & CO ELI.
 XX Bumol TF, Dou S, Glasebrook AL, Gould KE, Hale JE, Heuer JG;
 PI Hui KY, Kharitonov A, Mizrahi J, Na S, Noblitt TW, Reidy CA;
 PI Song HY, Wang J, Wu X, Zuckerman SH;
 XX WPI; 1999-591319/50.
 DR N-PSDB; AA225375.
 XX Use of mature FLINT for treating acute liver failure, inflammation,
 PT cancer, and diabetes - by prevention of FasL-Fas mediated apoptotic
 PT and proinflammatory activity
 XX Claim 30; Fig 1; 99pp; English.

XX The present invention describes therapeutic applications of mature FLINT
 CC (mFLINT) for use in the treatment of acute liver failure. Mature FLINT
 CC (mFLINT), which is a member of the tumour necrosis factor receptor
 CC superfamily, is used for treating acute liver failure, inflammation of
 CC the liver, abnormal hepatocyte apoptosis, sepsis, a disorder associated
 CC with inflammation, hepatitis, abnormal apoptosis, an ischaemia-associated
 CC injury or disorder such as hypercoagulation (including use with
 CC thrombolytic or anti-thrombolytic agents), reperfusion-associated injury
 CC or disorder, Type I diabetes, cancer, cell damage or damage to an
 CC innocent bystander tissue that is induced by a chemotherapeutic agent or
 CC therapeutic irradiation, treating haematopoietic progenitor cells that
 CC have been exposed to therapeutic radiation or chemotherapy, aplastic
 CC anaemia, myelodysplastic syndrome or a pancytopenic condition. mFLINT is
 CC also used for promoting the growth or differentiation of a haematopoietic
 CC progenitor cell or CD34+ cell and preventing damage to a cardiac myocyte
 CC resulting from abnormal myocardial ischaemia. The present sequence
 CC represents human FLINT.

XX SQ Sequence 300 AA;

Query Match 100.0%; Score 1491; DB 20; Length 300;
 Best Local Similarity 100.0%; Pred. No. 9.6e-115;
 Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 30 VAETPTYPWRDAETGERLVCAQCPGGTFVQPCRRDSPTTCGCPPRHYTFQWNYLERCR 89
 Qy 61 YCNVLCGEREEERACHATHNACRCRTGFFAHAGFCLEHASCPGAGVIAPGTPSQNTQ 120
 Db 90 YCNVLCGEREEERACHATHNACRCRTGFFAHAGFCLEHASCPGAGVIAPGTPSQNTQ 149
 Qy 121 CQPCPPGTFSSSSSQCPHRCNTALGLALNVPGSSSHDTLTCTSGTGPLSTRVPGAE 180
 Db 150 CQPCPPGTFSSSSSQCPHRCNTALGLALNVPGSSSHDTLTCTSGTGPLSTRVPGAE 209
 Qy 181 ECERAVIDFVAFQDISIKRLQLQLEAPEGNGTTPRAGRAALQLKRLRLTELLGAQD 240
 Db 210 ECERAVIDFVAFQDISIKRLQLQLEAPEGNGTTPRAGRAALQLKRLRLTELLGAQD 269
 Qy 241 GALLVRLQLALRVARMFGLERSVRERFLPVH 271
 Db 270 GALLVRLQLALRVARMFGLERSVRERFLPVH 300

RESULT 15

AAV17479

ID AAV17479 standard; Protein; 300 AA.

XX AC AAV17479;

XX 02-AUG-1999 (first entry)

XX Mammalian tumour necrosis factor receptor OPG-2.

XX Tumour necrosis factor receptor; TNF receptor; OPG-2; Paget's disease
KM Osteopenic disorder; osteoclast activity; primary osteoporosis;
KM hyperglycaemia; osteolytic metastasis; immune response; cancer.

hyperglycaemia; osteolytic metastasis; immune response; cancer.

hyperglycaemia; osteolytic metastasis; immune response; cancer.

OS Mamma.lia

PN WO9926977-A1

03-JUN-1999

24-NOV-1996; 98MO-0523063;
EF
XY

PR 24-NOV-1997: 97US-0066446

PA (BIOJ) BIOGEN INC.

PI Tschopp U;

DR WPI: 1999-347693/29

Now, remove the

PS Claim 1: Page 18: 23

CC The present sequence

CC factor receptor fami

The present sequence represents a mammalian tumour necrosis factor receptor, designated OPG-2. OPG-2, is a member of the tumour necrosis factor receptor family, and can be used: (i) to raise specific antibodies (Ab), (ii) to treat osteopenic disorders associated with excessive osteoclast activity, e.g. primary osteoporosis, Paget's disease, hyperglycaemia of malignancy, or osteolytic metastases; (iii) for affinity purification of cognate ligands, and (iv) to screen for ligands (antagonists or agonists). Ab, or other OPG-2 blocking agents such as soluble forms of the protein, are used to prevent, or reduce severity of, an immune response, and for treating cancer. They can also be used in diagnostic assays. The nucleic acid sequence encoding OPG-2 can be used as a probe to isolate related sequences from other species.

SQ Sequence 300 AA;

Best Local Similarity Query Match

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Search completed: 1/1/2011

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 6, 2003, 11:16:55 ; Search time 21 Seconds
(without alignments)
379.696 Million cell updates/sec

Title: US-09-936-024-1
Perfect score: 1491
Sequence: 1 VAETPTYPWRDAETGERLVC.....RVARMGLERSVREFLPVH 271

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	1491	100.0	300	2	US-08-794-796-2	Sequence 2, App1
2	1476.5	99.0	299	4	US-09-286-529-17	Sequence 17, App1
3	1034	69.3	211	4	US-09-286-529-20	Sequence 20, App1
4	841	56.4	153	4	US-09-286-529-2	Sequence 2, App1
5	440.5	29.5	401	3	US-08-974-022-6	Sequence 6, App1
6	440.5	29.5	401	4	US-09-042-785A-12	Sequence 12, App1
7	440.5	29.5	401	4	US-08-795-445A-6	Sequence 6, App1
8	440.5	29.5	401	4	US-08-795-447A-6	Sequence 6, App1
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29	385.5	25.9	364	4	US-08-706-945D-142	Sequence 142, App
30	374.5	25.1	364	4	US-08-706-945D-141	Sequence 141, App
31	373	25.0	139	4	US-08-706-945D-130	Sequence 130, App
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36	340.5	22.8	461	2	US-08-650-000-2	Sequence 2, App1
37	340.5	22.8	461	4	US-08-477-347-3	Sequence 3, App1
38	340.5	22.8	461	4	US-08-476-862-2	Sequence 2, App1
39	340.5	22.8	461	6	5395760-2	Patent No. 5395760
40	335	22.5	227	3	US-08-974-022-48	Sequence 48, App1
41	335	22.5	227	4	US-08-795-445A-48	Sequence 48, App1
42	335	22.5	227	4	US-08-795-447A-48	Sequence 48, App1
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45	335	22.5	227	4	US-08-706-945D-134	Sequence 134, App

ALIGNMENTS

RESULT 1
US-08-794-796-2
; Sequence 2, Application US/08794796
; Patent No. 5885800
; GENERAL INFORMATION:
; APPLICANT: Emery, John
; APPLICANT: Tan, KB
; APPLICANT: Truneh, Alem
; APPLICANT: Young, Peter
; TITLE OF INVENTION: Tumor Necrosis Related Receptor,
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSER: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/794,796
; FILING DATE: 04-FEB-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Han, William T
; REGISTRATION NUMBER: 34,344
; REFERENCE/DOCKET NUMBER: GH50000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5219
; TELEFAX: 610-270-4026
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 300 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-794-796-2
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RESULT 2
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; Sequence 17, Application US/09286529
; Patent No. 6297367
; GENERAL INFORMATION:
; APPLICANT: Catherine Triboulev
; TITLE OF INVENTION: NEW MEMBERS OF TNF AND TNFR FAMILIES
; FILE REFERENCE: 1408.003/200130.439C1
; CURRENT APPLICATION NUMBER: US/09/286,529
; CURRENT FILING DATE: 1999-04-05
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 17
; LENGTH: 299
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-286-529-17

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; Sequence 20, Application US/09286529
; Patent No. 6297367
; GENERAL INFORMATION:
; APPLICANT: Catherine Tribouley
; TITLE OF INVENTION: NEW MEMBERS OF TNF AND TNFR FAMILIES

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; FILE REFERENCE: 1408.003/200130.439C1
; CURRENT APPLICATION NUMBER: US/09/286,529
; CURRENT FILING DATE: 1999-04-05
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 20
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Best Local Similarity 98.9%; Pred. No. 4.8e-84;
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QY      1  VAETPTYPWRDAETGERLVCACQCPPGTFFVORPCRRDSPTTCGCPPRHYTQFWNYLERCR 60
Db      1  |||||
QY      30  VAETPTYPWRDAETGERLVCACQCPPGTFFVORPCRRDSPTTCGCPPRHYTQFWNYLERCR 89
Db      30  |||||
QY      61  YCNVLCGEREEERACHATHNACRCRTGFFAHAGFCLEHASCPPPGAGVIAPGTPSQNTQ 120
Db      61  |||||
QY      90  YCNVLCGEREEERACHATHNACRCRTGFFAHAGFCLEHASCPPPGAGVIAPGTPSQNTQ 149
Db      90  |||||
QY      121  CQCPRCCTFSASSSSSQCPHRCNTALGLALNVPGSSSHDTLCTCTCGPLSTRVPGAE 180
Db      121  |||||
QY      150  CQCPRCCTFSASSSSSQCPHRCNTALGLALNVPGSSSHDTLCTCTCGPLSTRVPGEP 209
Db      150  |||||

QY      181  E 181
Db      181  |

QY      210  E 210
Db      210  |

RESULT 4
US-09-286-529-2
; Sequence 2, Application US/09286529
; Patent No. 6297367
; GENERAL INFORMATION:
; APPLICANT: Catherine Tribouley
; TITLE OF INVENTION: NEW MEMBERS OF TNF AND TNFR FAMILIES
; FILE REFERENCE: 1408.003/200130.439C1
; CURRENT APPLICATION NUMBER: US/09/286,529
; CURRENT FILING DATE: 1999-04-05
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 153
; TYPE: PRT
; ORGANISM: human
; US-09-286-529-2

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Query Match          56.4%; Score 841; DB 4; Length 153;
Best Local Similarity 100.0%; Pred. No. 3.7e-67;
Matches 153; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  56  LERCYCNVLGGEREEBARACHATHNRCACRTGFFAHAGFCLEHASCPPGAGVIAFGTP 115
      |||||
Db  1  LERCYCNVLGGEREEBARACHATHNRCACRTGFFAHAGFCLEHASCPPGAGVIAFGTP 60
      |||||

Qy  116  SONTQOCPCPGGTFSSSSSECOCPHRNCTALGLALNVPGSSSHDTLCTCTGCGFPLSTR 175
      |||||
Db  61  SONTQOCPCPGGTFSSSSSECOCPHRNCTALGLALNVPGSSSHDTLCTCTGCGFPLSTR 120
      |||||

Qy  176  VPGAECERAVIDFVAFQDISIKRLQRLLOALE 208
      |||||
Db  121  VPGAECERAVIDFVAFQDISIKRLQRLLOALE 153
      |||||

RESULT 5
US-08-974-022-6
; Sequence 6, Application US/08974022
; Patent No. 6015938
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.

```

APPLICANT: Lacey, David L.
APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: OSTEOPROTEGERIN
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STREET: 1840 Dehavilland Drive
City: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,022
FILING DATE: 12-DEC-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/577,788
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-378
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 401 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-974-022-6

Query Match 29.5%; Score 440.5; DB 3; Length 401;
Best Local Similarity 41.2%; Pred. No. 2.9e-31;
Matches 77; Conservative 31; Mismatches 74; Indels 5; Gaps 2;

QY 5 PTYWRDAETGERLVCAQCPGPTGVORPCRRDSTPTGCPGPPRHYYTFWVYLERCRYCNV 64
DB 26 PKYHYDEBETSHOLCKCPGTYLKQHTAKMKTVCAPCPDHYTDSMHTSDCLYCSP 85
QY 65 LCGREBEARACHATNHRACRGTGFPFAHAGFCLHASCPRGAGVIAPTPSONTQOPC 124
DB 86 VCKELQYVKQECNTHNRVCEKGRYLEIEFLKHSRCPGFGVQAGTPERNTVCKRC 145
QY 125 PPGTFSSASSSSBQCPHRTCTALGLALNVPSSSHDTLCTSCGFFLSTRVPGAEE--C 182
DB 146 PDGFSNETSKAPCRKHTNCSVFGLLLTQGNATHDNI---CGNSSESTQKCGIDVTLC 202
QY 183 ERAVIDF 189
DB 203 EEAFFRF 209

RESULT 6
US-09-042-785A-12
Sequence 12, Application US/09042785A
Patent No. 6194151
GENERAL INFORMATION:
APPLICANT: Bufield, Samantha J
TITLE OF INVENTION: NOVEL MOLECULES OF THE TNF RECEPTOR SUPERFAMILY
TITLE OF INVENTION: AND USES THEREFOR
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
City: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/042,785A
FILING DATE: 17-MAR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/938,896
FILING DATE: 26-SEP-1997
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MEI-001CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 401 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-09-042-785A-12

Query Match 29.5%; Score 440.5; DB 4; Length 401;
Best Local Similarity 41.2%; Pred. No. 2.9e-31;
Matches 77; Conservative 31; Mismatches 74; Indels 5; Gaps 2;

QY 5 PTYWRDAETGERLVCAQCPGPTGVORPCRRDSTPTGCPGPPRHYYTFWVYLERCRYCNV 64
DB 26 PKYHYDEBETSHOLCKCPGTYLKQHTAKMKTVCAPCPDHYTDSMHTSDCLYCSP 85
QY 65 LCGREBEARACHATNHRACRGTGFPFAHAGFCLHASCPRGAGVIAPTPSONTQOPC 124
DB 86 VCKELQYVKQECNTHNRVCEKGRYLEIEFLKHSRCPGFGVQAGTPERNTVCKRC 145
QY 125 PPGTFSSASSSSBQCPHRTCTALGLALNVPSSSHDTLCTSCGFFLSTRVPGAEE--C 182
DB 146 PDGFSNETSKAPCRKHTNCSVFGLLLTQGNATHDNI---CGNSSESTQKCGIDVTLC 202
QY 183 ERAVIDF 189
DB 203 EEAFFRF 209

RESULT 7
US-08-795-445A-6
Sequence 6, Application US/08795445A
Patent No. 6284485
GENERAL INFORMATION:
APPLICANT: Boyle, William J.
APPLICANT: Lacey, David L.
APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: OSTEOPROTEGERIN
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STREET: 1840 Dehavilland Drive
City: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,445A
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA: 08/577,788
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-378
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 401 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-795-445A-6

	Query Match	29.5%; Score 440.5; DB 4; Length 401;
	Best Local Similarity	41.2%; Pred. No. 2.9e-31;
	Matches 77; Conservative 31; Mismatches 74; Indels 5; Gaps	
QY	5	PTVWRDAETGERLVCAQCPPGTFVQRRCRRDGPPTTCGPPRHHYTQFWNLYBCRYCINV 64
DB	26	PXVLHYDEEESHQLLCKDCPFGYLKHCHCTAKWKTVCAPCPDHYYTDSWHTSDECLYCSP 85
QY	65	LCSREBEARACHATHNNRACRCTGFPAHAGFCLFHASCPPGAGVIATPSTPSONTQCPC 124
DB	86	VKELQVVKOECNRTHRVCEKEGRYLEIFCLKHRSCPPFGVGVAQTPERNTVCKRC 145
QY	125	PCGTFSASSSSSEQPHRNCTALGLAIVNPVGSSSDTLCTSGTPPLSTRVPFCAGE--C 182
DB	146	PDGFFSNETSASKPCRKHNTCVSFGLLLTQGNATHDNI---CSGNSESIQKGIDVTLC 202
QY	183	ERAVIDF 189
DB	203	EAEFFRF 209

RESULT 8
US-08-795-447A-6
Sequence 6, Application US/08795447A
Patent No. 6284728
GENERAL INFORMATION:
APPLICANT: Boyle, William J.
APPLICANT: Lacey, David L.
APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: Osteoprotegerin
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STREET: One Amgen Center Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91362-1789
COMPUTER READABLE FORM:
MEDIA TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,447A
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-378D2
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 401 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-795-447A-6

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Query Match      29.5%; Score 440.5; DB 4; Length 401;
Best Local Similarity 41.2%; Pred. No. 2.9e-31;
Matches       77; Conservative 31; Mismatches    74; Indels     5; Gaps          6
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QY Db QY Db QY Db QY Db QY Db	<div></div> <div>5 PTVPRDAETGERLVCAQCPPGTFVORPCRRDSTPTTCGPCPPRHYTGFWNYLERCRCYNV 64</div> <div>26 PKLHUYDEESHQLCDKCPGGTYLVKHCHTAKWKTVCAPCPDRHHYTDSWHTSDECLYCSP 85</div> <div>65 LCGERBEARACHATHNRACRTGTFFAHAGFCLEHASCPPPGAGVIAPGPSONTOCQP 124</div> <div>86 VKCELQYVKOECRNTHNRVCEKEGRYLETEFCLKHRSCPPPGVVQAQTPERTVCKR 145</div> <div>125 PPGETSSASSSSSOCOPHRNCTALGLNALNVGPSSSHDTLTCTSGTPLSTRVPGAEE--C 182</div> <div>146 PDGPFNSNETSKAPCRKHTNCVSFGILLTKGNATHDNI---CSGNSESTQKGIDVTLC 202</div> <div>183 ERAVIDF 189</div> <div>203 EEAFFRF 209</div>
--	---

```
RESULT 9
US-08-974-186-6
; Sequence 6, Application US/08974186
; Patent No. 6284740
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: OSTEOPROTEGERIN
; NUMBER OF SEQUENCES:   53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatemIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,186
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/577,788
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-378
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 401 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-974-186-6
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	Query Match	29.5%	Score 440.5	DB 4	Length 401
	Best Local Similarity	41.2%	Pred. No. 2.9e-31		
	Matches	77	Conservative 31	Mismatches 74	Indels 5
					Gaps
Qy	5	PTYRWRDAETGERLVCACQCPGFGFVQPCRRDSTTCGCPPRHYTQFWNYLRCRCYCNV	64		
		: : : : :			
Db	26	PKYLHYDEETSHQLLCKCPGKYLKQCHTAKWTKVACPCDPDHYITDSMTTSECLYCSP	85		
		: : : : :			
Qy	65	LCGREREERACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTFPSQNTQCPC	124		
		: : : : :			

Db 86 VKCELQVYKQECNTHNRVCECKEGRYLEIFCLKHSCEPFGVQAGTBERNTVCRC 145
QY 125 PPGTSSASSSSSQCPHNRCTALGLANVPSSSHDTLCTSGTGFPLSTRVPAEE--C 182
Db 146 PDGFFSNETSXKAPCRKHTNCSVFGLLTLQKGNATHDNI---CGSNGSESTQKCGIDVTLC 202
QY 183 ERAVIDF 189
Db 203 EEAFFRF 209

RESULT 10
US-08-795-446B-6
; Sequence 6, Application US/08795446B
; Patent No. 6288032
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: OSTEOPROTEGERIN
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Dehaven Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/795,446B
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/577,788
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-378
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 401 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-795-446B-6

Query Match 29.5%; Score 440.5; DB 4; Length 401;
Best Local Similarity 41.2%; Pred. No. 2.9e-31;
Matches 77; Conservative 31; Mismatches 74; Indels 5; Gaps 2;

QY 5 PTYPMRDAETGERLIVCAQCPGTFVQRCRRDSPTTGCPCEPRHYTQPMYLERCRYCNV 64
Db 26 PKYLHYDEETSHQLCDKCPGYTLKQHTAKWTVCAPCPDHYTDSMTSDCLYCSP 85
QY 65 LCGREEREARACHATHNRACRGTGFPAHAGFCLEHASCSPGAGVIAPGTSSONTQOQC 124
Db 86 VKCELQVYKQECNTHNRVCECKEGRYLEIFCLKHSCEPFGVQAGTBERNTVCRC 145
QY 125 PPGTSSASSSSSQCPHNRCTALGLANVPSSSHDTLCTSGTGFPLSTRVPAEE--C 182
Db 146 PDGFFSNETSXKAPCRKHTNCSVFGLLTLQKGNATHDNI---CGSNGSESTQKCGIDVTLC 202
QY 183 ERAVIDF 189
Db 203 EEAFFRF 209

RESULT 11
US-09-153-927-1
; Sequence 1, Application US/09153927A
; Patent No. 6297022
; GENERAL INFORMATION:
; APPLICANT: McDonnell, Peter C.
; APPLICANT: Young, Peter R.
; APPLICANT: Zou, Jun
; TITLE OF INVENTION: A method of identifying agonists and
; TITLE OF INVENTION: Antagonists for Tumor Necrosis Related Receptors TR1, TR3
; FILE REFERENCE: GH50031
; CURRENT APPLICATION NUMBER: US/09/153,927A
; CURRENT FILING DATE: 1998-09-16
; EARLIER APPLICATION NUMBER: 60/061,334
; EARLIER FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Human
; US-09-153-927-1

Query Match 29.5%; Score 440.5; DB 4; Length 401;
Best Local Similarity 41.2%; Pred. No. 2.9e-31;
Matches 77; Conservative 31; Mismatches 74; Indels 5; Gaps 2;

QY 5 PTYPMRDAETGERLIVCAQCPGTFVQRCRRDSPTTGCPCEPRHYTQPMYLERCRYCNV 64
Db 26 PKYLHYDEETSHQLCDKCPGYTLKQHTAKWTVCAPCPDHYTDSMTSDCLYCSP 85
QY 65 LCGREEREARACHATHNRACRGTGFPAHAGFCLEHASCSPGAGVIAPGTSSONTQOQC 124
Db 86 VKCELQVYKQECNTHNRVCECKEGRYLEIFCLKHSCEPFGVQAGTBERNTVCRC 145
QY 125 PPGTSSASSSSSQCPHNRCTALGLANVPSSSHDTLCTSGTGFPLSTRVPAEE--C 182
Db 146 PDGFFSNETSXKAPCRKHTNCSVFGLLTLQKGNATHDNI---CGSNGSESTQKCGIDVTLC 202
QY 183 ERAVIDF 189
Db 203 EEAFFRF 209

RESULT 12
US-09-072-993C-1
; Sequence 1, Application US/09072993C
; Patent No. 6346388
; GENERAL INFORMATION:
; APPLICANT: Michael R. Bringham-Burke
; APPLICANT: Peter R. Young
; TITLE OF INVENTION: A METHOD OF IDENTIFYING AGONIST AND
; TITLE OF INVENTION: ANTAGONISTS FOR TUMOR NECROSIS RELATED RECEPTORS TR1 AND TR2
; FILE REFERENCE: GH-50030
; CURRENT APPLICATION NUMBER: US/09/072,993C
; CURRENT FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/055,513
; PRIOR FILING DATE: 1997-08-13
; PRIOR APPLICATION NUMBER: 60/056,980
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/057,550
; PRIOR FILING DATE: 1997-08-29
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 401
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
; US-09-072-993C-1

Query Match 29.5%; Score 440.5; DB 4; Length 401;
Best Local Similarity 41.2%; Pred. No. 2.9e-31;

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Matches 77; Conservative 31; Mismatches 74; Indels 5; Gaps 2;
QY 5 PTYPRDAETGERLVCAQCPGTFVQRPCCRDSPTTCGPPRRHYTQFWMYLERCRYCNV 64
Db 26 PKYLHYDEETSHQLLCKCPGTYLKQHCYKWKTVCAPCPDHYTDSWHTSDECLYCSP 85
QY 65 LCGEREEARACHATHNACRCRTGFFAHAGFCLEHASCPGAGVIAPGTPSNTQOQPC 124
Db 86 VKELQVVKQECNRTHNRVCECEGRYLETEFCLKHRSCPPGVLGVLQAGTPERNTVCKRC 145
QY 125 PPGTFASSSSSQOCPHRNCTALGLALNVPGSSSHDTLCTSGTGPLSTRVPGAEB--C 182
Db 146 PDGFFSNETSAPCRKHTNCSVFGLLLTQKGNATHDNI---CSGNSESTQKCGIDVTLC 202
QY 183 ERAVIDF 189
Db 203 EEAFFRF 209

RESULT 13
US-08-706-945D-128
; Sequence 128, Application US/08706945D
; Patent No. 6369027
; GENERAL INFORMATION:
; APPLICANT: Boyle, William
; APPLICANT: Lacey, David
; APPLICANT: Calzone, Frank
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: Osteoprotegerin
; FILE REFERENCE: A-378CIP
; CURRENT APPLICATION NUMBER: US/08/706, 945D
; CURRENT FILING DATE: 1996-09-03
; PRIOR APPLICATION NUMBER: 08/577,788
; PRIOR FILING DATE: 1995-12-22
; NUMBER OF SEQ ID NOS: 145
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 128
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-706-945D-128

Query Match 29.5%; Score 440.5; DB 4; Length 401;
Best Local Similarity 41.2%; Pred. No. 2.9e-31;
Matches 77; Conservative 31; Mismatches 74; Indels 5; Gaps 2;
QY 5 PTYPRDAETGERLVCAQCPGTFVQRPCCRDSPTTCGPPRRHYTQFWMYLERCRYCNV 64
Db 26 PKYLHYDEETSHQLLCKCPGTYLKQHCYKWKTVCAPCPDHYTDSWHTSDECLYCSP 85
QY 65 LCGEREEARACHATHNACRCRTGFFAHAGFCLEHASCPGAGVIAPGTPSNTQOQPC 124
Db 86 VKELQVVKQECNRTHNRVCECEGRYLETEFCLKHRSCPPGVLGVLQAGTPERNTVCKRC 145
QY 125 PPGTFASSSSSQOCPHRNCTALGLALNVPGSSSHDTLCTSGTGPLSTRVPGAEB--C 182
Db 146 PDGFFSNETSAPCRKHTNCSVFGLLLTQKGNATHDNI---CSGNSESTQKCGIDVTLC 202
QY 183 ERAVIDF 189
Db 203 EEAFFRF 209

RESULT 14
US-08-974-022-2
; Sequence 2, Application US/08974022
; Patent No. 601938
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: OSTEOPTROTEGERIN
```

```
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,022
; FILING DATE: 12-DEC-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/577,788
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-378
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 401 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-974-022-2

Query Match 28.5%; Score 425.5; DB 3; Length 401;
Best Local Similarity 39.5%; Pred. No. 6.2e-30;
Matches 81; Conservative 33; Mismatches 86; Indels 5; Gaps 2;
QY 5 PTYPRDAETGERLVCAQCPGTFVQRPCCRDSPTTCGPPRRHYTQFWMYLERCRYCNV 64
Db 26 PKYLHYDPETGROLLCDCKCAPGYLKQHCYKWKTVRRKTLVCPDYSYDTSWHTSDECLYCSP 85
QY 65 LCGEREEARACHATHNACRCRTGFFAHAGFCLEHASCPGAGVIAPGTPSNTQOQPC 124
Db 86 VKELQTVKQECNRTHNRVCECEGRYLETEFCLKHRSCPPGVLGVLQAGTPERNTVCKRC 145
QY 125 PPGTFASSSSSQOCPHRNCTALGLALNVPGSSSHDTLCTSGTGPLSTRVPGAEB--C 182
Db 146 PDGFFSGTSSKAPCRKHTNCSVLGLLLTQKGNATHDNI---CSGNREATQNCGIDVTLC 202
QY 183 ERAVIDFVAFQDISIKRLQRLQAL 207
Db 203 EEAFFRFAVPTKILPNWLSVLVDSL 227

RESULT 15
US-08-795-445A-2
; Sequence 2, Application US/08795445A
; Patent No. 6284485
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: OSTEOPTROTEGERIN
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
```

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,445A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/577,788
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-378
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 401 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-795-445A-2

Query Match 28.5%; Score 425.5; DB 4; Length 401;

Best Local Similarity 39.5%; Pred. No. 6, 2e-30;
Matches 81; Conservative 33; Mismatches 86; Indels 5; Gaps 2;

Qy 5 PTYPWRDAETGERLVCAQCPPGTFFVQRCRRDSPTTCGCPCPRHYYTQFMNYLERCRYCNV 64
Db 26 PKYLHYDPETGRQLCDKCAPGYLKHQCTVRRKTLCVPCPDYSYTDMSHTSDCVYCSP 85
Qy 65 LCGEREAEACHTHNRACRCRTGFFAHAGFCLEHASCPRGAGVIAPTPSQNTQCQPC 124
Db 86 VKELQTVKQECNRTHNRVCECEGRYLELEFCLKHRSCEPGLGLVLAQGTPERNTVCCKRC 145
Qy 125 PPGTFSSASSSSSECCPHRNCTALGLALNVGSSSHDTLCTSGTGFPLSTRVPGAE--C 182
Db 146 PDGFFSGETSSKAPCRGHTNCSSLGILLIQGNATHDNV---CSGNREATQNGSIDVTLC 202
Qy 183 ERAVIDFVAFODISIKRLRLQAL 207
Db 203 EBAFFRFVAVPTKIIPNWLVLVDSL 227

Search completed: January 6, 2003, 11:21:35
Job time : 22 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: January 6, 2003, 11:20:15 ; Search time 234 Seconds

(without alignments)
2608.064 Million cell updates/sec

Title: US-09-936-024-1

Perfect score: 1491

Sequence: 1 VAETPTPYRMDAETGRLVC.....RVAMRGLERSVVERFLPVH 271

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2185239 segs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-DB=N Geneseq.101002 -QMT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=bl0sum62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR SCORE=DCT -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NCM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USR=US09936024.@CGN_1.1.187@runcat.06012003_111606_12123 -NCP=6 -ICPU=3
-NO_XLXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREDS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

1: N_Geneseq.101002.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1491	100.0	813	20	AA225377
2	1491	100.0	813	21	AA25999
3	1491	100.0	813	21	AA88730
4	1491	100.0	813	21	AA51077
5	1491	100.0	813	22	AA07380
6	1491	100.0	813	24	AA27868
7	1491	100.0	900	20	AA225375
8	1491	100.0	900	21	AA53208
9	1491	100.0	900	21	AA51075
10	1491	100.0	903	20	AA22300
11	1491	100.0	903	22	AA33295
12	1491	100.0	1055	22	AA62705
13	1491	100.0	1066	21	AA53802
14	1491	100.0	1077	19	AAV39085
15	1491	100.0	1077	21	AA37772
16	1491	100.0	1077	24	AA33281
17	1491	100.0	1114	20	AA32744
18	1491	100.0	1114	21	AA58367
19	1491	100.0	1114	21	AA58581
20	1491	100.0	1114	21	AA77537
21	1491	100.0	1114	22	AA68421
22	1491	100.0	1114	22	AA91462
23	1491	100.0	1164	19	AAV07654
24	1491	100.0	1168	20	AA209998
25	1491	100.0	1179	22	AAH3171
26	1491	100.0	1205	20	AA07226
27	1491	100.0	1347	21	AA63764
28	1491	100.0	1428	21	AA53801
29	1491	100.0	1462	20	AA76052
30	1491	100.0	1550	24	AA23296
31	1485	99.6	825	20	AA25378
32	1485	99.6	825	21	AA51078
33	1485	99.6	936	20	AA25376
34	1477	99.1	1137	21	AA92404
35	1476	99.0	936	21	AA88731
36	1476	99.0	936	21	AA51076
37	1476	99.0	936	22	AA07385
38	1476	99.0	936	22	AA89920
39	1476	99.0	936	22	AA84738
40	1476	99.0	936	22	AA84739
41	1476	99.0	936	22	AA77696
42	1476	99.0	936	24	AA27869
43	1459.5	97.9	1224	24	AB055057
44	1384	92.8	900	21	AA53209
45	1339	89.8	1859	21	AA63765

ALIGNMENTS

RESULT 1
ID AA225377 standard; cDNA; 813 BP.
AC AA225377;
XX
XX 17-DEC-1999 (first entry)
DE Human mFLINT #1 nucleotide sequence.
XX
XX Human; FLINT; mFLINT; OP33; tumour necrosis factor receptor; FasL;
KW apoptosis; inflammation; cancer; diabetes; acute liver failure;
KW sepsis; hepatitis; ischaemia-associated injury; hypercoagulation;
KW reperfusion-associated injury; aplastic anaemia; differentiation;
KW growth; myelodysplastic syndrome; pancreatic condition;
KW myocardial ischaemia; ss.
XX
XX Homo sapiens.

XX WO9950413-A2.
 PN
 XX
 PD
 XX
 07-OCT-1999.
 PF
 XX
 30-MAR-1999; 99WO-US06797.
 XX
 30-MAR-1998; 98US-0079856.
 PR
 20-MAY-1998; 98US-0086074.
 PR
 09-SEP-1998; 98US-0099643.
 PR
 17-DEC-1998; 98US-0112577.
 PR
 18-DEC-1998; 98US-0112703.
 PR
 18-DEC-1998; 98US-0112933.
 PR
 22-DEC-1998; 98US-0113407.
 XX
 PA (ELIL) LILLY & CO ELI.
 XX
 PI Bumol TF, Dou S, Glasebrook AL, Gould KE, Hale JE, Heuer JG;
 PI Hui KY, Kharitonov A, Mizrahi J, Na S, Noblitt TW, Reidy CA;
 PI Song HY, Wang J, Wu X, Zuckerman SH;
 XX
 DR WPI; 1999-591319/50.
 DR P-PSDB; AA242184.
 XX
 PT Use of mature FLINT for treating acute liver failure, inflammation,
 PT cancer, and diabetes - by prevention of FasL-Fas mediated apoptotic
 PT and proinflammatory activity
 XX
 PS Claim 29; Fig 3; 99pp; English.
 XX
 CC The present invention describes therapeutic applications of mature FLINT
 CC (mFLINT) for use in the treatment of acute liver failure. Mature FLINT
 CC (mFLINT), which is a member of the tumor necrosis factor receptor
 CC superfamily, is used for treating acute liver failure, inflammation of
 CC the liver, abnormal hepatocyte apoptosis, sepsis, a disorder associated
 CC with inflammation, hepatitis, abnormal apoptosis, an ischaemia-associated
 CC injury or disorder such as hypercoagulation (including use with
 CC thrombolytic or anti-thrombolytic agents), reperfusion-associated injury
 CC or disorder, Type I diabetes, cancer, cell damage or damage to an
 CC innocent bystander tissue that is induced by a chemotherapeutic agent or
 CC therapeutic irradiation, treating haematopoietic progenitor cells that
 CC have been exposed to therapeutic radiation or chemotherapy, aplastic
 CC anaemia, myelodysplastic syndrome or a pancytopenic condition. mFLINT is
 CC also used for promoting the growth or differentiation of a haematopoietic
 CC progenitor cell or CD34+ cell and preventing damage to a cardiac myocyte
 CC resulting from abnormal myocardial ischaemia. The present sequence
 CC encodes human mFLINT.
 XX
 XX Sequence 813 BP; 122 A; 298 C; 267 G; 126 T; 0 other;
 SQ

Alignment Scores:
 Pred. No.: 3,46e-77 Length: 813
 Score: 1491.00 Matches: 271
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 20 Gaps: 0

US-09-936-024-1 (1-271) x AA253377 (1-813)

QY 1 ValAlaGluThrProThrTyrProThrArgAspAlaGluThrGlyGluArgLeuValCys 20
 DB 1 GTGGGAGAAACACCCACCTACCCCTCGCGGAGCGAGACAGCGGGCGGTGGTGC 60
 QY 21 AlaGlnCysProGlyThrPheValGlnArgProCysArgArgAspSerProThrThr 40
 DB 61 GCCAGTGCCCCCAGCAGCCTTTGTGTGACGGCCGTGCGCCGAGACAGCCCCACGAG 120
 QY 41 CysGlyProCysProProArgHisTyrThrGlnPheThrPAsnTyrLeuGluArgCysArg 60
 DB 121 TGTGGCCCGTGTCCACGGCCCACTACACGAGTTCCTGGAACCTACCTGGAGCGCTGCCG 180
 QY 61 TyrCysAsnValLeuGlyGluArgGluGluGluAlaArgAlaCysHisAlaThrHis 80

Db 181 TACTGCAACGTCCTCTCGGGGAGCGTGGAGGAGGCGCGGCTTGCACGCCACCCAC 240
 QY 81 AnArgAlaCysArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHis 100
 Db 241 AACCGTGTGCGCGTGGCGCACCGGCTTCTCGCGCACGCTGTGTTCTCTGTGGAGCAC 300
 QY 101 AlaSerCysProProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGln 120
 Db 301 GCATCGTGTCCACCTGGTGGCGGCTGATTGCCCCGGGACCCCCAGCAGACACGACG 360
 QY 121 CysGlnProCysProProGlyThrPheSerAlaSerSerSerSerSerGlnCysGln 140
 Db 361 TGCCAGCCGTGCCCCCAGGACCTTCTCAGCCACAGCTCCAGCTCAGAGCAGTGCCAG 420
 QY 141 ProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerSerHis 160
 Db 421 CCCCACCGCAACTGACGCGCCCTGGGCTGGCCCTCAATGTGCCAGGCTCTTCTCCCAT 480
 QY 161 AspThrLeuCysThrSerCysThrGlyPheProLeuSerThrArgValProGlyAlaGlu 180
 Db 481 CACACCTGTGCACAGCTGCACCTGGCTTCCCTCAGCAGCCAGGGTACCAGAGCTGAG 540
 QY 181 GluCysGluArgAlaValIleAspPheValAlaPheGlnAspIleSerIleLysArgLeu 200
 Db 541 GAGTGTGAGCGTGGCGTTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGTG 600
 QY 201 GlnArgLeuGlnAlaLeuGluAlaProGluGlyTTPGlyProThrProArgAlaGly 220
 Db 601 CAGCGGCTGTGCAGGCCCTCGAGGCCCGGAGGGCTGGGGTCCGACCAAGGGGGGCG 660
 QY 221 ArgAlaAlaLeuGlnLeuLysLeuArgArgLeuThrGluLeuLeuGlyAlaGlnAsp 240
 Db 661 CGCGCGGCTTGCAGCTGAAGCTGCGTGGCGGCTCAGCGAGCTCCTGGGGGCGCAGGAC 720
 QY 241 GlyAlaLeuValArgLeuGlnAlaLeuArgValAlaAlaArgMetProGlyLeuGlu 260
 Db 721 GGGGCGCTGTGTGGTGGCGTGTGTCAGGCGCTGCGGCTGGCCGAGGATGCCCGGGCTGGAG 780
 QY 261 ArgSerValArgGluArgPheLeuProValHis 271
 Db 781 CGAGCGTCCGTGAGCGCTTCTCTCCCTGTGCAC 813
 RESULT 2
 AAA75999
 ID AAA75999 standard; DNA; 813 BP.
 XX
 AC AAA75999;
 XX
 DT 19-FEB-2001 (first entry)
 XX
 DE DNA encoding a mature human FAS Ligand Inhibitory Protein (FLINT).
 KW Human; FAS Ligand Inhibitory Protein; FLINT; analogue; apoptosis;
 KW tumor necrosis factor receptor; acute lung injury; pulmonary fibrosis;
 KW acute respiratory distress syndrome; ulcerative colitis;
 KW chronic obstructive pulmonary disease; Crohn's disease; ss.
 XX
 OS Homo sapiens.
 XX
 FN WO200058465-A2.
 XX
 PD 05-OCT-2000.
 XX
 PF 20-MAR-2000; 2000WO-US06417.
 XX
 PR 30-MAR-1999; 99US-0126839.
 PR 21-JUN-1999; 99US-0140077.
 PR 21-JUN-1999; 99US-0140156.
 PR 20-OCT-1999; 99US-0160566.
 PR 18-FEB-2000; 2000US-0183398.
 XX
 PA (ELIL) LILLY & CO ELI.

XX Becker GW, Cohen FJ, Gonzalez-dewhitt PA, Hale JE, Micanovic R;
PI Newton CM, Noblitt TW, Rathmachalam R, Tschang SR, Witcher DR;
PI Wroblewski VJ;
XX WPI, 2000-6656167/63.
DR P-PSDB; AAB19334.
XX FAS ligand inhibitory Protein analogs useful for treating abnormal
PT apoptosis related diseases e.g. acute lung injury, pulmonary fibrosis,
PT chronic obstructive pulmonary disease ulcerative colitis or Crohn's
PT disease
XX
XX Claim 37, Page 113, 114pp; English.
XX
XX The present sequence encodes a mature human FAS ligand inhibitory
CC Protein (FLINT). FLINT is a homologue of tumour necrosis factor receptor
CC proteins. FLINT inhibits the binding of FAS to FAS ligand. The mature
CC FLINT protein is modified to produce analogues, which have greater
CC potency, longer in vivo half-lives, decreased aggregation, decreased
CC absorption onto surfaces, increased solubility and improved ease of
CC formulation. The FLINT analogue is useful for treating a patient
CC suffering from disease or condition relating to abnormal apoptosis such
CC as acute lung injury, acute respiratory distress syndrome, pulmonary
CC fibrosis, chronic obstructive pulmonary disease, ulcerative colitis, or
CC Crohn's disease.
XX
XX
SQ Sequence 813 BP; 122 A; 298 C; 267 G; 126 T; 0 other;

Alignment Scores:
Pred. No.: 3,46e-77 Length: 813
Score: 1491.00 Matches: 271
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 21 Gaps: 0

US-09-936-024-1 (1-271) x AAA75999 (1-813)

QY 1 ValAlaGluThrProThrTyProThrArgAspAlaGluThrGlyGluArgLeuValCys 20
Db 1 GTGGCAGAAACACCACTTACCTCTGGCGGAGCGAGACAGGGGAGCGCTGGTGGC 60
QY 21 AlaGlnCysProProGlyLThrPheValGlnArgProCysArgArgAspSerProThrThr 40
Db 61 GCCCAGTGTCCCGCCAGGACCTTTGTGCAAGCGCGCTGCCGCCAGACGCCACGACG 120
QY 41 CysGlyProCysProProArgHisLThrThrgLInpHeTIPaenTYLeuGluArgCysArg 60
Db 121 TGTGGCCCGTGTCCACGCGGCACACTACACGAGTTCTGGAACCTAGAGCGGTGGCGC 180
QY 61 TyrCysAsnValLeuCysGlyGluArgGluGluGluAlaAlaGlyCysHisAlaThrHis 80
Db 181 TACTGCAACGCTCTGTGGGGAGGTGAGAGAGGAGCGGCTTGGCAGCCACCCAC 240
QY 81 AsnArgAlaCysArgCysArgThrgLyphePheAlaHisAlaGlyPheCysLeuGluHis 100
Db 241 AACCTGCTTCCCGCTGCGCAGCGGCTTCTTCCGCGACGCTGTGTTTGTGGAGCAC 300
QY 101 AlaSerCysProProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrgLIn 120
Db 301 GCATCGTGTCCACCTGGGCGCGGTGATTGCCCGGGCAGCCCGCAGACAGACGCGAG 360
QY 121 CysGlnProCysProProGlyLThrPheSerAlaSerSerSerSerGlnGlnCysGln 140
Db 361 TGCAGCGGTGTCCCGCCAGGACCTTCTCAGCCAGCAGCTCCAGCTCAGACAGGCGCAG 420
QY 141 ProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerSerHis 160
Db 421 CCCACCGCACTGCACGCGCTGGGCTTGGCCCTCAATGTGCCAGGCTTCTTCCCAT 480
QY 161 AspThrLeuCysThrSerCysThrGlyPheProLeuSerThrArgValProGlyAlaGlu 180
|||||

Db 481 GACACCTGTGACACAGCTGCATGGCTTCCCTCAGCACACAGGATACAGAGCTGAG 540
QY 181 GluCysGluArgAlaValIleAspPheValAlaPheGlnAspIleSerIleLysArgHeu 200
Db 541 GAGTGTAGCTGCCGCTGCATGACTTTGTGCTTTCCAGGACATCTCCATCAAGAGCTTG 600
QY 201 GlnArgLeuLeuGlnAlaLeuGluAlaProGluGlyTyrGlyProThrProArgAlaGly 220
Db 601 CAGCGGCTGCTGCAGGCGCTCGAGCCCGGAGGCGTGGGCTCCGACACCAAGGCGCGC 660
QY 221 ArgAlaAlaLeuGlnLeuLysLeuArgArgArgLeuThrgLLeuLeuGlyAlaGlnAsp 240
Db 661 CGCGCGGCTTGCAGCTGAAGCTGCTCGCGGCTCAAGGAGCTCTGGGGCCAGGAC 720
QY 241 GlyAlaLeuLeuValArgLeuLeuGlnAlaLeuArgValAlaArgMetProGlyLeuGlu 260
Db 721 GGGCGCTGCTGTGCGGCTGCTGCTGAGCGCTGCGCGCTGGCAGAGGCGCGGCTGAG 780
QY 261 ArgSerValArgGluArgPheLeuProValHis 271
Db 781 CGAGCGCTCGTGAGCGCTTCTTCCCTGTGCAC 813

RESULT 3
AAA88730
ID AAA88730 standard; cDNA; 813 BP.
XX
AC AAA88730;
XX
DT 05-FEB-2001 (first entry)
XX
XX Human FAS ligand inhibitor protein FLINT cDNA.
DE
XX FLINT; FAS ligand inhibitory protein; human; protease resistant;
KW acute lung injury; acute respiratory distress syndrome;
KW chronic obstructive pulmonary disease; pulmonary fibrosis;
KW ulcerative colitis; therapy; organ transplantation; ss.
XX
XX Homo sapiens.
OS
XX
PN W0200058466-A2.
XX
PD 05-OCT-2000.
XX
PF 20-MAR-2000; 2000MO-US06418.
XX
PR 30-MAR-1999; 99US-0126839.
PR 21-JUN-1999; 99US-0140073.
PR 04-AUG-1999; 99US-0147071.
PR 20-OCT-1999; 99US-0160524.
PR 21-OCT-1999; 99US-0160669.
PR 20-DEC-1999; 99US-0172744.
PR 26-JAN-2000; 2000US-0178184.
XX
PA (BLIL) LILLY & CO ELI.
XX
PI Micanovic R, Rathmachalam R, Witcher DR;
XX WPI, 2000-664925/64.
DR P-PSDB; AAB19705.
XX
XX Novel protease resistant FAS ligand inhibitory protein analogues
PT resistant to in vivo or in vitro proteolysis at amino acid position 218
PT of the mature protein, useful for creating autoimmune diseases
XX
XX Disclosure; Page 95; 100pp; English.
XX
XX The present sequence is that of cDNA coding for human FAS ligand
CC inhibitory protein FLINT mature protein (see AAB19705). FLINT is a
CC tumour necrosis factor receptor homologue that binds FAS ligand,
CC preventing its interaction with FAS. This interaction is implicated
CC in runaway apoptosis and inflammatory disease. FLINT also binds to
CC LIGHT, a membrane-bound ligand, which may play a role in immune
CC modulation and apoptosis. The invention relates to novel FLINT

CC analogues (see also AAB19706-09) that are resistant to proteolysis
 CC by trypsin-like proteases between positions 218 and 219 of the
 CC FLINT mature protein sequence. Nucleic acids, vectors and
 CC transformed host cells for recombinant production of the analogues
 CC are claimed. FLINT cDNA is used as a template for introducing the
 CC required point mutations e.g. via PCR mutagenesis. The protease
 CC resistant FLINT analogues are used to prevent or treat acute lung
 CC injury, acute respiratory stress syndrome, ulcerative colitis,
 CC chronic obstructive pulmonary disease, pulmonary fibrosis, to
 CC inhibit T lymphocyte activation, and to facilitate organ
 CC preservation for transplantation (claimed).
 XX
 SQ Sequence 813 BP; 122 A; 298 C; 267 G; 126 T; 0 other;

Alignment Scores:

Pred. No.: 3,46e-77 Length: 813
 Score: 1491.00 Matches: 271
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 21 Gaps: 0

US-09-936-024-1 (1-271) x AAA88730 (1-813)

QY 1 ValAlaGluThrProThrTyrProThrArgAspAlaGluThrClyGluArgLeuValCys 20
 DB 1 GTGGCGAAGAACCCACCTACCCCTCGCGGGACGCAGACAGCGGGCGGTGGTGC 60
 QY 21 AlaGlnCysProProGlyThrPheValGlnArgProCysArgArgAspSerProThrThr 40
 DB 61 GCCAGTGTCCCCCAGCGACCTTTGTGACGGCGCTGCGCGCGAGACAGCCCCAGCG 120
 QY 41 CysGlyProCysProProArgHisTyrThrGlnPheThrAsnTyrLeuGluArgCysArg 60
 DB 121 TGTGGCCCGTGTCCACCGCGCCACTACACGAGTTCTGGAACCTACCTGGAGCGCTCCGC 180
 QY 61 TyrCysAsnValLeuCysGlyGluArgGluGluAlaAlaArgAlaCysHisAlaThrHis 80
 DB 181 TACTGCAACGTCTCTGCGGGAGCGTGTGAGGAGGCGCGCTTGCACGCCACCCAC 240
 QY 81 AsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHis 100
 DB 241 AACCGTGCTTGGCGTCCCGCACCGCGCTTCTTCGCGCACGCTGTTCTGTGGAGCAC 300
 QY 101 AlaSerCysProProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGln 120
 DB 301 GCATCGTGTCCACCTGGTGGCGCGTGAATTGCCCGGGCACCCCGCAGCAACACGCAG 360
 QY 121 CysGlnProCysProProGlyThrPheSerAlaSerSerSerSerSerSerSerSerSer 140
 DB 361 TGCCAGCCGTGCCCCCAGCGACCTTCTCAGCCAGCAGCTCCAGCTCAGCAGGTGCCAG 420
 QY 141 ProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerHis 160
 DB 421 CCCACCGCAACTGCACGGCCCTGGGCCCTCGCCCTCAATGTGCCAGGCTCTTCTCCCAT 480
 QY 161 AspThrLeuCysThrSerCysThrGlyPheProLeuSerThrArgValProGlyAlaGlu 180
 DB 481 GACACCTGTGCACACGAGTGCATGGCTTCCCCCTCAGCACACGAGGTACACGAGGTGAG 540
 QY 181 GluCysGluArgAlaValIleAspPheValAlaPheGlnAspIleSerIleCysArgLeu 200
 DB 541 GAGTGTGAGCGTCCGTCTATCGACTTGTGGCTTCCAGGACATCTCCATCAAGAGCGTG 600
 QY 201 GlnArgLeuGlnAlaLeuGluAlaProGluGlyTyrGlyProThrProArgAlaGly 220
 DB 601 CAGCGCTGTGTGAGCCCTTCGAGGCCCGGAGGGCTGGGGTCCGACACACAGGGCGGC 660
 QY 221 ArgAlaLeuGlnLeuLysLeuArgArgArgLeuThrGluLeuLeuGlyAlaGlnAsp 240
 DB 661 CGCGCGGCTTGCAGCTGAAGCTGCGTGCAGGCTCACGAGCTCTCTGGGGCGCAGGAC 720
 QY 241 GlyAlaLeuValArgLeuGlnAlaLeuArgValAlaArgMetProGlyLeuGlu 260

Db 721 GGGGCGCTGCTGCTGGCTGCTGCGAGCGCTGCGGTGCCAGGATGCCCGGGCTGGAG 780
 QY 261 ArgSerValArgGluArgPheLeuProValHis 271
 Db 781 CGGAGCGTCCGTGAGCGCTTCTCCCTGTGCAC 813
 RESULT 4
 AAA51077
 ID AAA51077 standard; DNA; 813 BP.
 XX
 AC AAA51077;
 XX
 DT 26-SEP-2000 (first entry)
 XX
 DE Mature human FLINT coding sequence.
 KW FLINT; osteoprotegrin 3; OPG3; tumour necrosis factor receptor; TNFR;
 KW FasL; LIGHT; apoptosis; pro-inflammatory; hepatotropic; vasotropic;
 KW anti-diabetic; anti-anaemic; neuroprotective; anti-ulcer; cytostatic;
 KW anti-inflammatory; antibacterial; immunosuppressive; ds.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT mat_peptide 1..813
 FT /*tag= a
 XX
 PN WO200037094-A2.
 PD 29-JUN-2000.
 XX
 PF 21-DEC-1999; 99WO-US30734.
 XX
 PR 22-DEC-1998; 98US-0113407.
 PR 30-MAR-1999; 99WO-US06797.
 PR 20-OCT-1999; 99US-0172239.
 XX
 PA (ELIL) LILLY & CO ELI.
 XX
 PI Cohen PJ, Posada JA, Wierda D;
 XX
 DR WPI; 2000-475441/41.
 DR P-PSDB; AAY96598.
 XX
 PT Use of mature FLINT for treating e.g. acute respiratory distress
 syndrome, ulcerative colitis or ischemic injury during organ
 transplantation
 XX
 PS Example 8; Fig 3A-B; 125pp; English.
 XX
 CC Human FLINT (also known as osteoprotegrin 3) is a new tumour necrosis
 factor receptor (TNFR) superfamily member, which binds FasL and LIGHT and
 prevents FasL-Fas interaction. Mature FLINT (mFLINT) inhibits FasL-Fas
 mediated apoptotic and pro-inflammatory activity. mFLINT is useful for
 treating acute respiratory distress syndrome, treating or inhibiting
 ulcerative colitis, inhibiting ischemic injury during organ
 transplantation or for organ preservation during transplantation. mFLINT
 can also be used to treat acute liver failure, inflammation of the liver,
 abnormal (hepatocyte) apoptosis, sepsis disorders associated with
 inflammation, hepatitis, ischemia, hypercoagulation or reperfusion,
 damage to a cardiac myocyte resulting from abnormal myocardial ischemia,
 Type I diabetes, cancer, damage to an innocent bystander tissue induced
 by a chemotherapeutic or therapeutic irradiation, aplastic anaemias,
 myelodysplastic syndromes and pancytopenic conditions.
 XX
 SQ Sequence 813 BP; 122 A; 298 C; 267 G; 126 T; 0 other;

Alignment Scores:

Pred. No.: 3,46e-77 Length: 813
 Score: 1491.00 Matches: 271
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0
 DB: 21 Gaps: 0
 US-09-936-024-1 (1-271) x AAAS1077 (1-813)

QY 1 ValAlaGluThrProThyTyrProTTPArgAspAlaGluThrGlyGluArgLeuValCys 20
 DB 1 GTGGCAAAACACCCACCCTTACCTCTGGGGAGACCAGACAGGAGGAGCGGCTGGTGC 60
 QY 21 AlaGlnCysProProGlyYThrPheValGlnArgProCysArgAspSerProThrThr 40
 DB 61 GCCAGAGTCCCCCAGAGCACTTTGTGACGCGTCCGCCAGACAGACGCCACGACG 120
 QY 41 CysGlyProCysProProArgHisTyrThrGlnPheThrAsnTyrLeuGluArgCysArg 60
 DB 121 TGTGGCCCGTGTCCACCGCGCCACTACACGAGTTCTGGAACTTCTGGACCGCTGCCG 180
 QY 61 TyrCysAsnValLeuCysGlyGluArgGluGluGluAlaArgGalaCysHisAlaThrHis 80
 DB 181 TACTGCAACGCTCTCTGCGGGAGCGTGAAGAGGAGGACGAGCGGCTTGGCCACGCCAC 240
 QY 81 AsnArgAlaCysArgCysArgThyGlyPhePheAlaHisAlaGlyPheCysLeuGluHis 100
 DB 241 AACCGTCCCTGCGCGTCCGACCGGCTTCTTCCGCAACGCTGTTCTTGGAGACAC 300
 QY 101 AlaSerCysProProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGln 120
 DB 301 GCATCGTGTCCACTGTGTGCGGGCTGATTCGCCGGACACCCACAGACAAACAGCAG 360
 QY 121 CysGlnProCysProProGlyYThrPheSerAlaSerSerSerSerSerGluGlnCysGln 140
 DB 361 TGCACGCGGTGCCCCCAGGACCTTCTCACGCCAGACTCCAGACTCAGACAGTGCAG 420
 QY 141 ProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerSerHis 160
 DB 421 CCCACGCGCACTGACAGCGCTGCGCTGCGCTCAATGCGCAGGCTCTTCCCTCCAT 480
 QY 161 AsnThrLeuCysThrSerCysThrGlyPheProLeuSerThrArgValProGlyValAlaGlu 180
 DB 481 GACACCTGTGTCACACGACTGCACTGGCTTCCCCCTCAGACACAGGAGTACAGAGCTGAG 540
 QY 181 GluCysGluArgAlaValIleAspPheValAlaPheGlnAspIleSerIleLeuArgLeu 200
 DB 541 GAGGTGAGCGTCCGCTCATGACTTGTGGCTTCCAGGACATCTCATCAAGAGGCTG 600
 QY 201 GlnArgLeuLeuGlnAlaLeuGlnAlaProGluGlyTTPGlyProThrProArgAlaGly 220
 DB 601 CAGCGCTGTGTCAGGCGCTTCGAGGCCCCGAGGAGGCTGGGGTCCGACACCAAGGCGGGC 660
 QY 221 ArgAlaAlaLeuGlnLeuLeuArgArgArgLeuThrGluLeuGluValAlaGlnAsp 240
 DB 661 CGCGCGGCTTGGACGCTGAGCTGAGCTGCGGCGCTCAGCGAGGCTCTGGGGGCGCAGGAC 720
 QY 241 GlyAlaLeuLeuValArgLeuLeuGlnAlaLeuArgValAlaArgMetProGlyLeuGlu 260
 DB 721 GGGGCGTGTGCGGCGCTGCTGCAAGCGCTGCGCGGCGGCGCAGAGATGCCGGGCTGAG 780
 QY 261 ArgSerValArgGluArgPheLeuProValHis 271
 DB 781 CGAGCGCTCCGTGAGCGCTTCTCCCTGTCGAC 813

RESULT 5
 AAD07380
 ID AAD07380 standard; cDNA; 813 BP.
 XX AAD07380;
 AC
 XX 04-AUG-2001 (first entry)
 DT
 XX Human mature fas ligand inhibitory protein (FLINT) cDNA.
 DE Human, fas ligand inhibitory protein; FLINT; acute lung injury; ALI;
 XX Human, fas ligand inhibitory protein; FLINT; acute lung injury; ALI;
 KW Human, fas ligand inhibitory protein; FLINT; acute lung injury; ALI;
 KW TNFR; tumour necrosis factor receptor protein; ulcerative colitis; ARDS;

KM acute respiratory distress syndrome; pulmonary fibrosis; PF; therapy;
 KM chronic obstructive pulmonary disease; COPD; acute lung injury; goitre;
 KM rheumatoid arthritis; fibropoliferative lung disease; ischaemia; sepsis;
 KM fibrotic lung disease; human immunodeficiency virus; HIV; osteoporosis;
 KM chronic renal failure; graft-vs-host disease; cutaneous inflammation;
 KM vascular leak syndrome; Helicobacter pylori infection; atherosclerosis;
 KM insulin dependent diabetes mellitus (IDDM); inflammatory bowel disease;
 KM Crohn's disease; pancreatitis; cancer; autoimmune disease; psoriasis;
 KM Down's syndrome; multiple sclerosis; cytostatic; nocrotic;
 KM neuroprotective; vasotropic; ss.
 XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
 FH 1..813
 FT CDS /tag= a
 FT /product= "Human mature fas ligand inhibitory protein
 FT (FLINT)"
 FT /note= "CDS does not include start and stop codon"
 FT /partial
 XX MO200142463-AL.
 XX 14-JUN-2001.
 XX 29-NOV-2000; 2000MO-US30166.
 XX PF 07-DEC-1999; 99US-0169367.
 XX PR 07-DEC-1999; 99US-0169381.
 XX PR 07-DEC-1999; 99US-0169412.
 XX PR 23-MAR-2000; 2000US-0191430.
 XX (ELIL) LILLY & CO ELI.
 XX Lu J, Wilcher DR;
 XX WPI: 2001-381684/40.
 XX P-PSDB; AAB03567.
 XX New FLINT polypeptide for treating and/or preventing acute lung injury,
 PT acute respiratory distress syndrome, ulcerative colitis, and
 PT graft-versus-host disease, comprises O-linked or N-linked
 PT oligosaccharides -
 XX
 XX Example 1; Page 53; 60pp; English.
 PS The present sequence is human mature fas ligand inhibitory protein
 CC (FLINT) cDNA. FLINT, a homologue of tumour necrosis factor receptor
 CC protein (TNFR), binds fas ligand (FasL) and thereby preventing the
 CC interaction of FasL with Fas. FLINT comprising O-linked or N-linked
 CC oligosaccharides is useful for preventing or treating acute lung injury
 CC (ALI), acute respiratory distress syndrome (ARDS), ulcerative colitis,
 CC chronic obstructive pulmonary disease (COPD) and pulmonary fibrosis (PF),
 CC to facilitate organ preservation for transplantation and to inhibit T
 CC lymphocyte activation. FLINT is useful for treating and/or preventing
 CC diseases such as rheumatoid arthritis, fibropoliferative lung disease,
 CC fibrotic lung disease, acute lung injury, human immunodeficiency virus
 CC (HIV), ischaemia, brain trauma/injury, chronic renal failure, graft-vs-
 CC host disease, cutaneous inflammation, vascular leak syndrome,
 CC Helicobacter pylori infection, goitre, atherosclerosis, insulin dependent
 CC diabetes mellitus (IDDM), osteoporosis, inflammatory bowel disease,
 CC Crohn's disease, sepsis, pancreatitis, cancer, autoimmune disease such as
 CC psoriasis, Down's syndrome, and multiple sclerosis.
 XX
 XX Sequence 813 BP; 122 A; 298 C; 267 G; 126 T; 0 other;
 SQ

Alignment Scores:
 Pred. No.: 3 46e-77 Length: 813
 Score: 1491.00 Matches: 271
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 22 Gaps: 0

US-09-936-024-1 (1-271) x AAD07380 (1-813)

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QY 1 ValAlaGluThrProThrTyrProTrpArgAspAlaGluThrGlyGluArgLeuValCys 20
Db 1 GTGGGAGAAACACCCACCTACCCCTGGCGGACGACAGACAGGGGAGCGGTGGTGTGC 60
QY 21 AlaGlnCysProGlyThrPheValGlnArgProCysArgAspSerProThrThr 40
Db 61 GCCCAGTCCCCCAGGACCTTTGTGACGGCCGTGCCGCGACAGACAGCCACGACG 120
QY 41 CysGlyProCysProProArgHisTyrThrGlnPheTrpAsnTyrLeuGluArgCysArg 60
Db 121 TGTGGCCCTGTCTCCACCGGCCACTACAGCAGTCTTGGAACTACCTGGAGCGCTCCGC 180
QY 61 TyrCysAsnValLeuCysGlyGluArgGluGluAlaArgAlaCysHisAlaThrHis 80
Db 181 TACTGCAAGTCTCTGCGGGAGCGTGGAGGAGGACGCGGCTTGGCCACGCCACCCAC 240
QY 81 AsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHis 100
Db 241 AACCGTGTGCGCGCTGCCGACCGCTTCTTCGCGCACGCTGCTTCTGTTGGAGCAC 300
QY 101 AlaSerCysProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGln 120
Db 301 GCATCGTGTCCACCTGTGCGCGCGTGAATTGCCCGCGGACCCCGGACAGCAGCAG 360
QY 121 CysGlnProCysProGlyThrPheSerAlaSerSerSerSerGluGlnCysGln 140
Db 361 TGGCAGCGTGGCCCCCAGGACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTCCAG 420
QY 141 ProHisArgAsnThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerHis 160
Db 421 CCCCACGCAACTGCACGCGCTTGGCGCTTCAATGTGCGAGGCTCTTCTCCCAT 480
QY 161 AspThrLeuCysThrSerCysThrGlyPheProLeuSerThrArgValProGlyAlaGlu 180
Db 481 GACACCTGTGACACAGCTGCACCTGCTTCCCGCTCAGCACCAGGTTACGAGAGCTGAG 540
QY 181 GluCysGluArgAlaValIleAspPheValAlaPheGlnAspIleValArgLeu 200
Db 541 GAGTGTGAGGTCGCTCATCGACTTGTGGCTTTCAGGACATCTCCATCAGAGGCTG 600
QY 201 GlnArgLeuLeuGlnAlaLeuGluAlaProGluGlyTrpGlyProThrProArgAlaGly 220
Db 601 CACGCGCTGTCTGACGCGCTCGAGGCCCCGCGGCGCTGGGTCGACACACCAAGGGCGGC 660
QY 221 ArgAlaAlaLeuGlnLeuLysLeuArgArgLeuThrGluLeuLeuGlyAlaGlnAsp 240
Db 661 CGCGCGCTTGTGAGCTGAAGCTGCGTGGCGGCTCACGAGCTCTCGGGGCGCGAGAC 720
QY 241 GlyAlaLeuLeuValArgLeuLeuGlnAlaLeuArgValAlaArgMetProGlyLeuGlu 260
Db 721 GGGCGCTGTGTGGCTGTCTGCGGCTGTCTGAGGCGCTGCGGCTGCGGAGATGCCGGGCTGGAG 780
QY 261 ArgSerValArgGluArgPheLeuProValHis 271
Db 781 CGGAGCTCGTGTGAGCGCTTCTCCCTCGTGTGCAC 813
```

RESULT 6

AAD27868

ID AAD27868 standard; DNA; 813 BP.

XX

AC AAD27868;

XX

DT 01-JUL-2002 (first entry)

XX

DE Human mature FLINT DNA.

XX

KW FLINT; FAS ligand inhibitory protein; pulmonary; lung; apoptosis;

KW organ failure; liver; kidney; pancreas; inflammatory disease;

KW neutrophil; sepsis; acute respiratory distress syndrome;

KW acute lung injury; systemic inflammatory response syndrome; SIRS;

KW multiple organ dysfunction; MODS; human; gene; ds.

XX Homo sapiens.

OS

XX

PH Key

FT CDS

FT

FT

FT

FT

XX

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multiple organ dysfunction; MODS; human; gene; ds.
Homo sapiens.
Key Location/Qualifiers
CDS 1..813
/*tag= a
/product= "Mature FLINT protein"
/note= "Does not include start and stop codons"
/partial

XX WO200209668-A2.

XX 07-FEB-2002.

XX

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Administering FLINT (FAS ligand inhibitory protein) or FLINT analog, useful for treating e.g. sepsis or respiratory distress syndrome, involves pulmonary administration of a therapeutic amount of the FLINT or FLINT analog -

Disclosure; Page 30; 35pp; English.

The invention relates to a new method of administering FLINT (FAS ligand inhibitory protein) or FLINT analog that involves pulmonary administration of a therapeutic amount of the FLINT or FLINT analog. The method enables systemic absorption of FLINT through lungs and significantly reduces or eliminates the need for administering FLINT by injection or other routes of administration. The method is useful in treating disorders related to enhanced apoptosis (e.g. organ failure in liver, kidneys and pancreas) and inflammatory diseases associated with neutrophil activation (e.g. sepsis, acute respiratory distress syndrome, acute lung injury, systemic inflammatory response syndrome (SIRS) and multiple organ dysfunction (MODS)). The method minimises the pain and discomfort of injection methods. The present sequence is human mature FLINT DNA.

SQ Sequence 813 BP; 122 A; 298 C; 267 G; 126 T; 0 other;

Alignment Scores:

Pred. No.:	3,46e-77	Length:	813
Score:	1491.00	Matches:	271
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	24	Gaps:	0

US-09-936-024-1 (1-271) x AAD27868 (1-813)

QY 1 ValAlaGluThrProThrTyrProTrpArgAspAlaGluThrGlyGluArgLeuValCys 20
Db 1 GTGGGAGAAACACCCACCTACCCCTGGCGGACGACAGACAGGGGAGCGGTGGTGTGC 60
QY 21 AlaGlnCysProGlyThrPheValGlnArgProCysArgAspSerProThrThr 40
Db 61 GCCCAGTCCCCCAGGACCTTTGTGACGGCCGTGCCGCGACAGACAGCCACGACG 120
QY 41 CysGlyProCysProProArgHisTyrThrGlnPheTrpAsnTyrLeuGluArgCysArg 60
Db 121 TGTGGCCCTGTCTCCACCGGCCACTACAGCAGTCTTGGAACTACCTGGAGCGCTCCGC 180
QY 61 TyrCysAsnValLeuCysGlyGluArgGluGluAlaArgAlaCysHisAlaThrHis 80
Db 181 TACTGCAAGTCTCTGCGGGAGCGTGGAGGAGGACGCGGCTTGGCCACGCCACCCAC 240

[illegible]

22-DEC-1998; 98US-0113407.
 (EHLI) LILLY & CO ELI.
 BunoI TF, Dou S, Glasbrook AL, Gould KE, Hale JE, Heuer JG;
 Hui KY, Kharitonovskoy A, Mizrahi J, Na S, Noblitt TW, Reidy CA;
 Song HY, Wang X, Wu X, Zuckerman SH;
 WPI; 1999-591319/50.
 P-PSDB; AAY42182.
 Use of mature FLINT for treating acute liver failure, inflammation,
 cancer, and diabetes - by prevention of FasL-Fas mediated apoptotic
 and proinflammatory activity
 Claim 28; Fig 1, 99p; English.
 The present invention describes therapeutic applications of mature FLINT
 (mFLINT) for use in the treatment of acute liver failure. Mature FLINT
 (mFLINT), which is a member of the tumour necrosis factor receptor
 superfamily, is used for treating acute liver failure, inflammation of
 the liver, abnormal hepatocyte apoptosis, sepsis, a disorder associated
 with inflammation, hepatitis, abnormal apoptosis, an ischaemia-associated
 injury or disorder such as hypercoagulation (including use with
 thrombolytic or anti-thrombolytic agents), reperfusion-associated injury
 or disorder, Type I diabetes, cancer, cell damage or damage to an
 innocent bystander tissue that is induced by a chemotherapeutic agent or
 therapeutic irradiation, treating haematopoietic progenitor cells that
 have been exposed to therapeutic radiation or chemotherapy, aplastic
 anaemia, myelodysplastic syndrome or a pancytopenic condition. mFLINT is
 also used for promoting the growth or differentiation of a haematopoietic
 progenitor cell or CD34+ cell and preventing damage to a cardiac myocyte
 resulting from abnormal myocardial ischaemia. The present sequence
 encodes human FLINT.
 Sequence 900 BP; 128 A; 324 C; 304 G; 144 T; 0 other;
 Alignment Scores:
 Pred. No.: 3,85e-77 Length: 900
 Score: 1491.00 Matches: 271
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 20 Gaps: 0
 US-09-936-024-1 (1-271) x AA225375 (1-900)
 QY 1 ValAlaGluThrProThrTyrrProTIPaRgAsPaLagIuThngIuArgLeuValCys 20
 Db 88 GTGGCAAAACACCCACCTACCCCTGGCGGAGACGAGAGACGGGGAGCGCTGGTGGC 147
 QY 21 AlaGlnCysProProGlyThrPheValGlnAArgProCybAgaRgAsPserProThrThr 40
 Db 148 GCCCAGAGCCCCCAGGACCTTTGGCAGCGCGCGCTGGCGCGGACAGCCACGACG 207
 QY 41 CysGlyProCysProProArgHisTyrrThngInPheTpaNtyrLeuGlnArgCysArg 60
 Db 208 TGTGGCCCGGTGTCCACCGCGCCACTACAGCGAGTTCTGGAACTACTTGGACGGCTGGCGC 267
 QY 61 TyrCysAsnValLeuCysGlyGluArgGlnGlnGlnAlaArgAlaCysHisAlaThrHis 80
 Db 268 TACTGCAAGCTCTCTGGCGGGAGCGGTAGAGAGAGGACGGGGCTTGGCAAGCCACCAC 327
 QY 81 AsnArgAlaCysArgCysArgThrglyPhePheAlaHisAlaGlyPheCysLeuGlnHis 100
 Db 328 AACCGTCCCGCGCGCGCGCACCGCGCTTCTTGGCGACCGCTGTCTTGGAGAC 387
 QY 101 AlaSerCysProProGlyAlaGlyValIleAlaProGlyYthrProSerGlnAsnThrGln 120
 Db 388 GCATGTGTCCACCTGT 447
 QY 121 CysGlnProCysProProGlyThrPheSerAlaSerSerSerSerSerSerSerSerSerSer 140

Db 448 TGCCAGCGTGCCTCCAGCAGCAGCTTCTCAGCCAGCAGCTCCAGCTCAGCAGTCCAG 507
 Qy 141 ProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerHis 160
 Db 508 CCCACCGCAACTGCACGCGCTGGCCCTCAATGTGCAGGCTCTTCTCCCAT 567
 Qy 161 AspThrLeuCysThrSerCysThrGlyPheProLeuSerThrArgValProGlyAlaGlu 180
 Db 568 GACACCTGTGCACCACTGCAGCTGGCTTCCCTCAGCACCAGGTTACCGAGCTGAG 627
 Qy 181 GluCysGluArgAlaValIleAspPheValAlaPheGlnAspIleSerIleLysArgGlu 200
 Db 628 GAGTGTAGCGTCCGCTCATGCTTGGCTTTCAGGACATCTCCATCAGAGGCTG 587
 Qy 201 GlnArgLeuLeuGlnAlaLeuGluAlaProGluGlyTrpGlyProThrProArgAlaGly 220
 Db 688 CAGCGCTGTGCAGGCCCTCGAGGCCCGGAGGCTGGGGTCCGACCAAGGGCGGC 747
 Qy 221 ArgAlaAlaLeuGlnLeuLysLeuArgArgLeuThrGluLeuLeuGlyAlaGlnAsp 240
 Db 748 CGCGCGCTTGCAGCTGAAGCTGCGTGGCGCTCAGCAGCTCCTGGGGCGCAGGAC 807
 Qy 241 GlyAlaLeuValArgLeuLeuGlnAlaLeuArgValAlaArgMetProGlyLeuGlu 260
 Db 808 GGGCGCTGTGTGGCGCTGCTGCAGGCGCTGCGGTGGCCAGGATGCCCGGCTGGAG 867
 Qy 261 ArgSerValArgGluArgPheLeuProValHis 271
 Db 868 CGGAGGCTCGTGCAGCGCTTCTCCCTCCCTGTGCAC 900
 RESULT 8
 ID AAA53208
 AC AAA53208 standard; cDNA; 900 BP.
 XX
 AC AAA53208;
 XX
 DT 03-JAN-2001 (first entry)
 XX
 DE Human Fas ligand inhibitor FLINT coding sequence.
 XX
 KW Human; Fas ligand inhibitor; FLINT; apoptosis; autoimmune disease;
 KW inflammation; infectious disease; ischaemia; Alzheimer's disease;
 KW Parkinson's disease; Crohn's disease; transplantation; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..900
 FT /*tag= a
 FT /product= "FLINT"
 FT /partial
 FT sig_peptide 1..90
 FT /*tag= b
 FT mat_peptide 91..900
 FT /*tag= c
 XX
 PP WO200034782-A1.
 XX
 PD 15-JUN-2000.
 XX
 PF 07-DEC-1999; 99WO-US28696.
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 PR 09-DEC-1998; 98US-0111575.
 PR 09-DEC-1998; 98US-0111580.
 PR 07-JAN-1999; 99US-0115069.
 XX
 PA (ELIL) LILLY & CO ELI.
 XX
 PI Rosteck PRJ, Song HY, Su EW;
 XX
 DR WPI: 2000-431379/37.
 DR P-PSDB; AAB03621.
 XX

PT Novel monkey Fas ligand inhibitor polypeptides, useful for treating
 PT inflammatory or autoimmune disease such as rheumatoid arthritis,
 PT infectious diseases such as chronic hepatitis, and
 XX ischaemia/Re-perfusion conditions -
 PS Example 1; Page 88-91; 101pp; English.
 XX
 CC The present sequence is the coding sequence of the human Fas ligand
 CC inhibitor (FLINT). The FLINT protein is involved in cell-specific
 CC apoptosis, and can be used to treat inflammatory and autoimmune diseases
 CC such as rheumatoid arthritis, inflammatory bowel disease,
 CC graft-versus-host disease, diabetes, psoriasis and Graves' disease.
 CC infectious diseases such as HIV-induced lymphopenia, fulminant viral
 CC hepatitis B/C, chronic hepatitis and cirrhosis, and H. pylori-associated
 CC ulceration, ischaemia and reperfusion conditions including acute
 CC myocardial infarction, acute coronary syndrome, congestive heart failure
 CC and atherosclerosis, and Alzheimer's and Parkinson's diseases, acute lung
 CC injury and acute respiratory distress syndrome, Crohn's disease, brain
 CC trauma and injury, chronic glomerulonephritis, osteoporosis, aplastic
 CC anaemia, myelodysplasia, ulcerative colitis, Down's syndrome, and
 CC multiple sclerosis. In addition, the gene and protein can be used to
 CC prevent apoptosis following organ transplantation.
 XX
 SQ Sequence 900 BP; 128 A; 324 C; 304 G; 144 T; 0 other;
 Alignment Scores:
 Pred. No.: 3.85e-77 Length: 900
 Score: 1491.00 Matches: 271
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 21 Gaps: 0
 US-09-936-024-1 (1-271) x AAA53208 (1-900)
 Qy 1 ValAlaGluThrProThrTyrProTrpArgAspAlaGluThrGlyGluArgLeuValCys 20
 Db 88 GTGGCAGAAACACCCACCTTACCCCTGGCGGGACGAGAGAGGGGAGCGGTGGTGTGC 147
 Qy 21 AlaGlnCysProGlyThrPheValGlnArgProCysArgAspSerProThrThr 40
 Db 148 GCCAGTGGCCCCCAGGACCTTTGTGCAGCGCGCTGCCCGCGAGACAGCCCCAGCAG 207
 Qy 41 CysGlyProCysProProArgHisTyrThrGlnPheTrpAsnTyrLeuGluArgCysArg 60
 Db 208 TGTGGCCCGTGTCCACCGCGCCACTACACGCACTTCTGGAACCTACCTGAGCGCTGCC 267
 Qy 61 TyrCysAsnValLeuCysGlyGluArgGluGluAlaArgAlaCysHisAlaThrHis 80
 Db 268 TACTCAACGCTCTCTGGCGGAGCGTGGAGGAGGCGACCGGCTTGGCCACCCACCCAC 327
 Qy 81 AsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHis 100
 Db 328 AACCGTGCCTGCGCTGCCGACCGGCTTCTTCGCGCAGCGTGGTTCCTGCTTGGAGC 387
 Qy 101 AlaSerCysProProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGln 120
 Db 388 GCATCGTGTCCACCTGTCGCGCGCTGATTGCCCGGGGACCCGCCAGCAGCAACACG 447
 Qy 121 CysGlnProCysProGlyThrPheSerAlaSerSerSerSerSerSerSerSerSer 140
 Db 448 TGCCAGCGCTGCCCGCCCGGACCTTCTCAGCCAGCAGCTCCAGCTCAGAGAGTCCAG 507
 Qy 141 ProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerHis 160
 Db 508 CCCACCGCAACTGCACGCGCTGGCCCTCAATGTGCAGGCTCTTCTCCCAT 567
 Qy 161 AspThrLeuCysThrSerCysThrGlyPheProLeuSerThrArgValProGlyAlaGlu 180
 Db 568 GACACCTGTGCACCACTGCAGCTGGCTTCCCTCAGCACCAGGTTACCGAGCTGAG 627
 Qy 181 GluCysGluArgAlaValIleAspPheValAlaPheGlnAspIleSerIleLysArgGlu 200

Dh 628 GAGGTGAGCGTCCGTCATGACTTGTGGCTTTCCAGACATCTCCATCAAGAGCGTG 687
Qy 201 GlnArgLeuLeuGlnAlaLeuGlnAlaProGlnGlyTTPGlyProThrProArgAlaGly 220
Dh 688 CAGGGCGTGTGCGAGCGCTCGAGGCCCGGAGGGCTGGGGTCCGACGCCAAGGGCGGCG 747
Qy 221 ArgAlaAlaLeuGlnLeuLeuLeuArgArgArgLeuThrGlnLeuLeuGlyAlaGlnAsp 240
Dh 748 CGCGCGGCTTGACGTGAGCTGCTGCGCGCTCAAGGAGCTCTGGGGCGCAGGAC 807
Qy 241 GlnAlaLeuLeuValArgLeuLeuGlnAlaLeuArgValAlaArgMetProGlyLeuGln 260
Dh 808 GGGGCGTGTGCGGCGCTGCTGAGGCGCTGCGCGCTGCGCAGAGTCCGCGCTGGAG 867
Qy 261 ArgSerValArgGlnArgPheLeuProValHis 271
Dh 868 CGAGCGTCCCTGAGCGCTTCTCTCTGTGAC 900
RESULT 9
AAAS1075
ID AAAS1075 standard; DNA; 900 BP.
XX
AC AAAS1075;
XX
DT 26-SEP-2000 (first entry)
XX
DE Human FLINT coding sequence.
XX
KW FLINT, osteoprotegerin 3; OPG3, tumour necrosis factor receptor; TNFR;
KW FasL; LIGHT; apoptosis; pro-inflammatory; hepatotropic; vasotropic;
KW anti-diabetic; anti-anemic; neuroprotective; anti-ulcer; cytostatic;
KW anti-inflammatory; antibacterial; immunosuppressive; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..900
FT /*tag= a
FT /product= FLINT
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FT sig_peptide 1..87
FT /*tag= b
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FT /*tag= c
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PN MO200037094-A2.
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XX 29-JUN-2000.
PD
XX 21-DEC-1999; 99WO-US30734.
PF
XX 22-DEC-1998; 98US-0113407.
PR 30-MAR-1999; 99WO-US06797.
PR 20-OCT-1999; 99US-0172239.
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PA (EHLI) LILLY & CO ELI.
XX
PI Cohen FJ, Posada JA, Wierda D;
XX
XX MPI; 2000-475441/41.
DR P-PSDB; AAY96596.
XX
PT Use of mature FLINT for treating e.g. acute respiratory distress
PT syndrome, ulcerative colitis or ischemic injury during organ
PT transplantation
XX
XX Example 7; Fig 1A-B; 125pp; English.
PS
XX Human FLINT (also known as osteoprotegerin 3) is a new tumour necrosis
CC factor receptor (TNFR) superfamily member, which binds FasL and LIGHT and
CC prevents FasL-Fas interaction. Mature FLINT (mFLINT) inhibits FasL-Fas
CC mediated apoptotic and pro-inflammatory activity. mFLINT is useful for
CC treating acute respiratory distress syndrome, treating or inhibiting

CC ulcerative colitis, inhibiting ischemic injury during organ
CC transplantation or for organ preservation during transplantation. mFLINT
CC can also be used to treat acute liver failure, inflammation of the liver,
CC abnormal (hepatocyte) apoptosis, sepsis, disorders associated with
CC inflammation, hepatitis, ischemia, hypercoagulation or reperfusion,
CC damage to a cardiac myocyte resulting from abnormal myocardial ischemia,
CC Type I diabetes, cancer, damage to an innocent bystander tissue induced
CC by a chemotherapeutic or therapeutic irradiation, aplastic anaemias,
CC myelodysplastic syndromes and pancytopenic conditions.
XX
SQ Sequence 900 BP; 128 A; 324 C; 304 G; 144 T; 0 other:
Alignment Scores:
Pred. No.: 3.85e-77 Length: 900
Score: 1491.00 Matches: 271
Percent Similarity: 100.00% Conservative: 0
Best local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 21 Gaps: 0
US-09-936-024-1 (1-271) x AAAS1075 (1-900)
Qy 1 ValAlaGlnThrProThrTyrProTyrArgAspAlaGlnThrGlyGlnArgLeuValCys 20
Dh 88 GTGGCAGAAACACCCACCTACCCCTGGGGGACCGACAGACAGGGGAGCGGCTGTGTGC 147
Qy 21 AlaGlnCysProProGlyThrPheValGlnArgProCysArgAspSerProThrThr 40
Dh 148 GCCAGTGCCTCCCGGACCTTTGTGACGGCGGCTGCCCCGACAGACAGCCACGACG 207
Qy 41 CysGlyProCysProProArgHisTyrThrGlnPheThrPheThrTyrLeuGlnArgCysArg 60
Dh 208 TGTGGCCCGTGTCCACCGCGCCCACTACACGAGTTCTGGAATCACTCTGGAGCGTGGCCG 267
Qy 61 TyrCysAsnValLeuCysGlyGlnArgGlnGlnAlaArgAlaCysHisAlaThrHis 80
Dh 268 TACTGCAACGTCCTCTGTGGGGAGCGTGGAGAGAGGACGGGCTTGGCAAGCCAC 327
Qy 81 AsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGlnHis 100
Dh 328 AACGTCCTGCGCTGCGGACCGGCTTCTTGGCAGCGGTGTTCTGTGGAGCAC 387
Qy 101 AlaSerCysProProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGln 120
Dh 388 GCATCGTGTCCACCTGGTGGCGGGGTATGTCGCCGGGACCCCAAGCACAACACGACG 447
Qy 121 CysGlnProCysProProGlyThrPheSerAlaSerSerSerSerSerGlnCysGln 140
Dh 448 TGCCAGCGGTGCCCCCAGGACCTTCTCAGCCAGACCTCAGACCTCAGACGAGTGGCAG 507
Qy 141 ProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerSerHis 160
Dh 508 CCCACCGCAACTGACAGCGCTGCGCTGCGCTGCAATGTCAGAGGCTCTTCCCAT 567
Qy 161 AspThrLeuCysThrSerCysThrGlyPheProLeuSerThrArgValProGlyAlaGln 180
Dh 568 GACACCTGTGTGACACAGTGTGAGTGTCTTCCCTCAGCACAAGGATCCAGAGCTGAG 627
Qy 181 GlnCysGlnArgAlaValIleAspPheValAlaPheGlnAspIleSerIleLeuArgLeu 200
Dh 628 GAGTGTGAGCGTGCCTGTCATGACCTTGTGTGCTTCCAGGACATCTCATCAAGAGCTG 687
Qy 201 GlnArgLeuLeuGlnAlaLeuGlnAlaProGlnGlyTTPGlyProThrProArgAlaGly 220
Dh 688 CAGCGCGTGTGAGCGCTTCCAGGCGCCCGGAGGAGCTGGGGTCCGACCCAAGGGCGGCG 747
Qy 221 ArgAlaAlaLeuGlnLeuLeuLeuArgArgArgLeuThrGlnLeuLeuGlyAlaGlnAsp 240
Dh 748 CGCGCGGCTTGACGTGAGCTGCTGCGCGCTCAAGGAGCTCTGGGGCGCAGGAC 807
Qy 241 GlnAlaLeuLeuValArgLeuLeuGlnAlaLeuArgValAlaArgMetProGlyLeuGln 260
Dh 808 GGGGCGTGTGCGGCTGCTGAGGCGCTGCGCGCTGCGCAGAGTCCGCGGCTGGAG 867

QY 261 ArgSerValArgGluArgPheLeuProValHis 271
 Db 868 CGAGCGGTCGTCGAGCGCTTCTCCCTGTGCAC 900

RESULT 10

AAAX22300
 ID AAX22300 standard; DNA; 903 BP.

AC AAX22300;

DT 20-MAY-1999 (first entry)

XX Orphan receptor (HUMAN NTR-1) polypeptide encoding DNA.

XX HUMAN NTR-1; orphan receptor; osteoprotegerin; OPG; TNFR; human;
 KW tumour necrosis factor receptor; muscle disorder; bone mass; screening;
 KW muscle metabolism; binding agent; cognate ligand; ss.

XX Homo sapiens.

XX WO9907738-A2.

XX 18-FEB-1999.

XX 04-AUG-1998; 98WO-US16202.

XX 06-AUG-1997; 97US-0054869.

XX (PROC) PROCTER & GAMBLE CO.

XX (REG-) REGENERON PHARM INC.

XX Mastakowski PJ, Morris J, Valenzuela DM;

XX WPI; 1999-167365/14.

XX P-PSDB; AAW95082.

XX Novel orphan human receptor polypeptide and nucleic acid - useful as
 PT diagnostic reagents and for treatment of muscle disorders

XX Claim 2; Page 21; 23pp; English.

XX This DNA encodes a HUMAN NTR-1 polypeptide, a novel orphan receptor. The
 CC protein is related to osteoprotegerin (OPG) and to tumour necrosis factor
 CC receptor (TNFR). Host cells transformed with a vector comprising the
 CC HUMAN NTR-1 nucleic acid are used for the recombinant expression of the
 CC protein. HUMAN NTR-1 proteins and antibodies immuno specific for the
 CC protein are useful for diagnosis and treatment of humans and animals,
 CC especially muscle disorders, as the receptor is involved in regulation of
 CC bone mass and muscle metabolism. HUMAN NTR-1 receptors are also useful
 CC for screening for novel binding agents, and cognate ligands, which may be
 CC used to treat disorders associated with HUMAN NTR-1 imbalance.

XX SQ Sequence 903 BP; 129 A; 324 C; 305 G; 145 T; 0 other;

Alignment Scores:

Pred. No.: 3,86e-77 Length: 903
 Score: 1491.00 Matches: 271
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 20 Gaps: 0

US-09-936-024-1 (1-271) x AAX22300 (1-903)

QY 1 ValAlaGluThrProThrTyrProTrpArgAspAlaGluThrGlyGluArgLeuValCys 20
 Db 88 GTGGCGAAACACCCACTACCTCGCGGAGCGAGACAGCGGGCGGTGGTGC 147

QY 21 AlaGlnCysProProGlyThrPheValGlnArgProCysArgArgAspSerProThrThr 40
 Db 148 GCCCAGTGCCTCCCGCAGGCACCTTTGTGACGGCGGTGCGCGGAGACAGCCCGACGAGC 207

QY 41 CysGlyProCysProProArgHisTyrThrGlnPheTrpAsnTyrLeuGluArgCysArg 60
 Db 208 TGTGGCCCGTGTCCACCGCGCACTACACGCGAGTTCTGGAACTACCTGGAGCGCTGCCGC 267
 QY 61 TyrCysAsnValLeuCysGlyGluArgGluGluGluAlaAtrGAlaCysHisAlaThrHis 80
 Db 268 TACTGCACAGTCTCTTGGGGAGCGGTGAGGAGGAGGACCGGGCTTGCACGCCACCCAC 327
 QY 81 AsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHis 100
 Db 328 AACCGTGCCTGCGCGTCCGCGCACCGGCTTCTTCGCGCACGCTGGTTCTCTGTGGAGCAC 387
 QY 101 AlaSerCysProProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGln 120
 Db 388 GCATCGTGTCCACCTGTGTCGGCGGTGATTGCCCGGGCACCCCGCAGCAGAACACGCAG 447
 QY 121 CysGlnProCysProProGlyThrPheSerAlaSerSerSerSerSerGluGlnCysGln 140
 Db 448 TGCCAGCGGTGCCCCCGGCGACCTTCTCAGCCAGAGCTCCAGCTCAGAGCAGTGCCAG 507
 QY 141 ProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerHis 160
 Db 508 CCCCACCGCAACTGCAACGCGCTGCGGCTGCGCTCAATGTGCCAGGCTCTTCTCCCAT 567
 QY 161 AspThrLeuCysThrSerCysThrGlyPheProLeuSerThrArgValProGlyAlaGlu 180
 Db 568 GACACCTGTGCACAGCTGCACCTGGCTTCCCTCAGCACCGAGGTACAGAGCTGAG 627
 QY 181 GluCysGluArgAlaValIleAspPheValAlaPheGlnAspIleSerIleLeuArgLeu 200
 Db 628 GAGTGTGAGCGTGGCGTCAATCGACTTTGGCTTTCCAGGACATCTCCATCAAGAGGCTG 687
 QY 201 GlnArgLeuLeuGlnAlaLeuGluAlaProGluGlyTyrGlyProThrProArgAlaGly 220
 Db 688 CAGCGGCTGTGCGAGGCTCTCAGGCGCGGAGGCTGGGTCCGACACCAAGGCGGCG 747
 QY 221 ArgAlaAlaLeuGlnLeuLysLeuArgArgArgLeuThrGluLeuLeuGlyAlaGlnAsp 240
 Db 748 CGCGCGGCTTGCAGCTGAAGCTGCGTGGCGGCTCAGCGAGCTCTCTGGGGCGCGAGGAC 807
 QY 241 GlyAlaLeuLeuValArgLeuLeuGlnAlaLeuArgValAlaAlaArgMetProGlyLeuGlu 260
 Db 808 GGGGCGCTCTGTGCGGCTGTGCGAGGCTGCGCGTGGCCAGGATGCCGGGCTGGAG 867
 QY 261 ArgSerValArgGluArgPheLeuProValHis 271
 Db 868 CGGAGGCTCCGTGAGGCTTCTCTCCCTGTGCAC 900

RESULT 11

AAAD3295

ID AAD3295 standard; DNA; 903 BP.

XX AAD3295;

XX 01-JUL-2002 (first entry)

XX Mammalian synthetic tumour necrosis factor receptor (TNFR)-6alpha DNA.
 DE Tumour necrosis factor receptor; TNFR-6alpha; TNFR-6beta; therapy;
 KW immune system-related disorder; inflammatory disease; immunosuppressive;
 KW bowel disease; encephalitis; atherosclerosis; gastrointestinal-Gen;
 KW autoimmune disease; systemic lupus erythematosus; rheumatoid arthritis;
 KW multiple sclerosis; Crohn's disease; autoimmune encephalitis; allergy;
 KW graft versus host disease; GVHD; antiinflammatory; psoriasis; arthritis;
 KW neuroprotective; antiarteriosclerotic; dermatological; asthma; receptor;
 KW gene; ds.

XX Mammalia.

OS Synthetic.

XX WO200218622-A2.

XX 07-MAR-2002.

XX 24-AUG-2001; 2001WO-US26396.
 PF 25-AUG-2000; 2000US-227598P.
 XX 21-NOV-2000; 2000US-252131P.
 PR 06-JUL-2001; 2001US-303224P.
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA
 XX Gentz RL, Edner R, Yu G, Ruben SM, Ni J, Feng P;
 PI WPI; 2002-281068/32.
 DR
 XX Novel nucleic acid molecules comprising a polynucleotide encoding human
 PT tumor necrosis factor receptor (TNFR)-galpha and 6beta polypeptides
 PT useful for treating disease e.g. inflammatory and autoimmune disorders
 PT
 XX Claim 37; Page 348; 350pp; English.
 PS
 XX The invention relates to human tumour necrosis factor receptor (TNFR) -
 CC 6alpha and 6beta protein and their corresponding nucleic acids. The
 CC invention provides screening methods for identifying agonists and
 CC antagonists of TNFR-6alpha and 6beta activity. The invention also
 CC provides diagnostic and therapeutic methods for detecting and treating
 CC immune system-related disorders. The method is useful for treating or
 CC preventing an inflammatory disease or disorder selected from bowel
 CC disease, encephalitis, atherosclerosis and psoriasis, an autoimmune
 CC disease or disorder selected from systemic lupus erythematosus,
 CC arthritis, rheumatoid arthritis, multiple sclerosis, Crohn's disease,
 CC and autoimmune encephalitis, graft versus host disease (GVHD), and an
 CC allergy or asthma. The present sequence is Mammalian synthetic TNFR-
 CC 6alpha DNA.
 CC
 XX
 SQ Sequence 903 BP; 171 A; 253 C; 265 G; 214 T; 0 other;

Alignment Scores:
 Pred. No.: 3.86e-77 Length: 903
 Score: 1491.00 Matches: 271
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 24 Gaps: 0

US-09-936-024-1 (1-271) x AAD33295 (1-903)

QY 1 ValAlaGluThrProThrTyrProTyrArgAspAlaGluThrGlyGluArgLeuValCys 20
 DB 88 GTGGCTGAAACACCTACATATCCATGAGAGATGCTGAAACAGGAAGGCTGTGTGT 147

QY 21 AlaGlnCysProProGlyThrPheValGlnArgProCysArgArgAspSerProThrThr 40
 DB 148 GCTAGAGTCTCTCTGGAAACATTTGTGCAAGGCTGTAGCGGATCTCTCAACGACG 207

QY 41 CysGlyProCysProProArgHisTyrThrGlnPheThrPasnTyrLeuGluArgCysArg 60
 DB 208 TGTGGCCCTTGCCCTCTAGGCACTATACACAGTTTGGAACTATCTCGAGCCCTGAGG 267

QY 61 TyrCysAsnValLeuGlyGluArgGluGluGluAlaArgAlaCysHisAlaThrHis 80
 DB 268 TATGCAACGCTCTCTGGAGAAAGGAGAGAGCAAGCGCTTGTTCATGCAACACAC 327

QY 81 AsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHis 100
 DB 328 AACAGGGGATGTAGGTGTGCGACAGGCTTCTTGTCTCATGCTGAGATTTTGTCTGAAAC 387

QY 101 AlaSerCysProProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGln 120
 DB 388 GCTTCTTGTCTCTCTGGGTGAGAGTATGCTCTCTGTATACACCTCTCAACAACACCA 447

QY 121 CysGlnProCysProProGlyThrPheSerAlaSerSerSerSerGluGlnCysGln 140
 DB 448 TGCAGGCTGTCTCTCTGGGACCTTCTCTGCACTATGCTTCACCTCTGAAACAATGCGAA 507

QY 141 ProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerSerHis 160
 DB 508 CTTACCGGCATTTTACAGCTCTGGAGCTGGCTCTGAAACGCTGTGTTCTCTCCCAT 567

QY 161 AspThrLeuCysThrSerCysThrGlyPheProLeuSerThrArgValProGlyAlaGlu 180
 DB 568 GATACCTGTGTACACAGCTGACTGCTTCTCTCTACCCGCGTGGCGCTGAA 627

QY 181 GlucyGluArgAlaValIleAspPheValAlaPheGlnAspIleSerIleValArgLeu 200
 DB 628 GAGTGCACAGCGCTGTGATGACTTGTGCTTCCAGGATATCTATCAAAAGGCTG 687

QY 201 GlnArgLeuLeuGlnAlaLeuGluAlaProGluGlyTyrGlyProThrProArgAlaGly 220
 DB 688 CAAGCGCTGCTGCAAGCTCTGGAAGCTCTGAGGGCTGGGCTCCCAACCAAGGGCTGC 747

QY 221 ArgAlaAlaLeuGlnLeuLysLeuArgArgArgLeuThrGluLeuGlyAlaGlnAsp 240
 DB 748 AGGCTGCACCTGCAACTGAGAGCTTCGACAGAGGCTCACTGAACTCTGGAGCTCAAGAT 807

QY 241 GlyAlaLeuLeuValArgLeuLeuGlnAlaLeuArgValAlaArgMetProGlyLeuGlu 260
 DB 808 GGAAGCTGTGCTGTGAGGCTGTGCAAGCTCTGAGGGTGGCAAGAGCTTGAGACTGGAG 867

QY 261 ArgSerValArgGluArgPheLeuProValHis 271
 DB 868 CGCTCTGTGAGGAGACGCTTCTCTGCTGTGCAC 900

RESULT 12
 AAF62705
 ID AAF62705 standard; cDNA; 1055 BP.
 XX
 AC AAF62705;
 XX
 DT 02-MAY-2001 (first entry)
 XX
 XX Human NTR3 nucleotide sequence.
 DE
 XX Human; NTR3; tumour necrosis factor receptor; TNF receptor; anti-HIV;
 KM antianaemic; immunosuppressive; antidiabetic; antiviral; antibacterial;
 KM cytoskeletal; neuroprotective; antiinflammatory; anorectic; vasotropic;
 KM antirheumatoid; antiarthritic; cerebroprotective; tuberculostatic;
 KM gene therapy; cancer; blood disorder; brain disorder; autoimmune disease;
 KM infection; ss.
 KW
 XX Homo sapiens.
 OS
 XX NC0200110908-A1.
 FN
 XX PD 15-FEB-2001.
 XX
 XX 02-AUG-2000; 2000WO-US21287.
 PF
 XX 04-AUG-1999; 99US-0147297.
 PR
 XX (AMGE-) AMGEN INC.
 PA
 XX Heu H;
 PI
 XX WPI; 2001-191521/19.
 DR P-PSDB; AAB71754.
 DR
 PT New tumor necrosis factor receptor, NTR3, useful for treating cancers,
 PT stroke, anemia, obesity, rheumatoid arthritis and transplantation
 PT rejection -
 PT
 XX
 PS Claim 1; Page 128-129; 135pp; English.
 XX
 CC The present sequence encodes the tumour necrosis factor (TNF) receptor
 CC polypeptide NTR3. The NTR3 polynucleotides and polypeptides are useful
 CC for treating diseases such as acquired-immunodeficiency syndrome (AIDS),
 CC anaemia, autoimmune diseases, cachexia, cancer, cerebral malaria,

CC diabetes mellitus, disseminated intravascular coagulopathy, erythroid
 CC sick syndrome, haemorrhagic shock, hepatitis, insulin resistance.
 CC leprosy, leukaemia, meningitis, multiple sclerosis, myocardial ischaemia,
 CC obesity, rejection of transplanted organs, rheumatoid arthritis, septic
 CC shock syndrome, stroke, adult respiratory distress syndrome (ARDS),
 CC tuberculosis, and a number of viral diseases. The NTR3 polypeptide is
 CC useful for identifying or developing new (ant)agonists of NTR3. It may
 CC be used as an immunogen to which antibodies may be raised. NTR3 nucleic
 CC acid molecules may be useful as hybridisation probes in diagnostic assays
 CC to test, either qualitatively or quantitatively, for the presence of an
 CC NTR3 DNA or corresponding RNA in mammalian tissue or bodily fluid
 CC samples.
 XX

SQ Sequence 1055 BP; 160 A; 369 C; 340 G; 186 T; 0 other;

Alignment Scores:

Pred. No.: 4 54e-77 Length: 1055
 Score: 1491.00 Matches: 271
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 22 Gaps: 0

US-09-936-024-1 (1-271) x AAF62705 (1-1055)

QY 1 ValAlaGluThrProThrTyProTrpArgAspAlaGluThrGlyGluArgLeuValCys 20
 Db 154 GTGGAGAAACACCCACTACCTCCCTGGCGGACGACAGACAGGGAGCGCTGGTGTGC 213
 QY 21 AlaGlnCysProGlyThrPheValGlnArgProCysArgAspSerProThrThr 40
 Db 214 GCCAGTGCCTCCCGCAGCACCTTTGTGCAGCGCGGTGGCGGACAGACAGCCACGACG 273
 QY 41 CysGlyProCysProArgHisTyThrGlnPheTrpAsnTyThrLeuGluArgCysArg 60
 Db 274 TGTGGCCCGTGTCCACCGCGCCACTACACGAGTTCTGGAACTACCTGGAGCGCTGCCGC 333
 QY 61 TyxCysAsnValLeuCysGlyGluArgGluGluAlaAlaGluAlaCysHisAlaThrHis 80
 Db 334 TACTGCAACGTCTCTCGCGGGAGCGTGAGGAGGACCGGCTTGCCACAGCCACCCAC 393
 QY 81 AsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHis 100
 Db 394 AACCGTCCCTGCCGCTGCCGACCGGCTTCTTCGCGCACGCTGGTTCTCTGGAGCAC 453
 QY 101 AlaserCysProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGln 120
 Db 454 GCATCGTGTCCACTGTGTGGCGGTGATTGCCCCGGGACCCCGCCAGCCAGAACAGCGAG 513
 QY 121 CysGlnProCysProGlyThrPheSerAlaserSerSerSerGluGlnCysGln 140
 Db 514 TGCCAGCGTGCCTCCCGCAGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCGTGCAG 573
 QY 141 ProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerSerHis 160
 Db 574 CCCACCGCAACTGCACGCGCCCTGGGCGCTGAGCTTTCAGGACATCTCCATCAAGAGCTG 633
 QY 161 AspThrLeuCysThrSerCysThrGlyPheProLeuSerThrArgValProGlyAlaGlu 180
 Db 634 GACACCTGTGCACCACTGCATCGCTTCCCTCTGACACAGGGTACAGAGCTGAG 693
 QY 181 GluCysGluArgAlaValIleAspPheValAlaPheGlnAspIleSerIleCysArgLeu 200
 Db 694 GAGTGTGAGCGTGGCGTCATCGCTTGTGGCTTTCAGGACATCTCCATCAAGAGCTG 753
 QY 201 GlnArgLeuLeuGlnAlaLeuGluAlaProGluGlyTrpGlyProThrProArgAlaGly 220
 Db 754 CAGCGGTGTGTGAGGCGCTCGAGCGCCCGGAGGCGTGGGGTCCGACCAAGCGCGGC 813
 QY 221 ArgAlaAlaLeuGlnLeuLysLeuArgArgLeuThrGluLeuLeuGlyAlaGlnAsp 240
 Db 814 CGCGCGGCTTGCAGCTGAGAGTGTGCTGGCGGCTCAGGAGCTCTCTGGGGGCGCAGGAC 873

QY 241 GlyAlaLeuValArgLeuGlnAlaLeuArgValAlaArgMetProGlyLeuGlu 260
 Db 874 GGGGGCGCTCTGTCGGCTGCTGCAGGCGCTGCAGGATGCCGCTGCCAGATGCCGGCTGGAG 933
 QY 261 ArgSerValArgGluArgPheLeuProValHis 271
 Db 934 CGGAGCGTCCGTGAGCGCTTCTCTCCCTGTGCAC 966
 RESULT 13
 AAAS3802
 ID AAAS3802 standard; cDNA; 1066 BP.
 XX
 AC AAAS3802;
 XX
 DT 19-DEC-2000 (first entry)
 XX
 DE M68 TNF receptor related protein coding sequence.
 XX
 KW M68; tumour necrosis factor; TNF; programmed cell death; apoptosis;
 KW receptor; immune response; cell differentiation; ligand; cancer;
 KW bone disease; systemic lupus erythematosus; Hashimoto's thyroiditis;
 KW Grave's disease; idiopathic myxedema; autoimmune diabetes;
 KW thrombotic thrombocytopenic purpura; multiple sclerosis;
 KW liver diseases; autoimmune gastritis; ulcerative colitis;
 KW glomerulonephritis; pulmonary fibrosis; heart failure;
 KW atherosclerosis; aplastic anaemia; myelodysplastic syndromes;
 KW osteoporosis; Alzheimers disease; parkinsons disease; stroke;
 KW myocardial infarction; human; ds.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 CDS 53..955
 FT /*tag= a
 FT /product= M68 polypeptide
 XX
 FN WO200046247-A1.
 XX
 PD 10-AUG-2000.
 XX
 PF 04-FEB-2000; 2000WO-US03037.
 XX
 PR 05-FEB-1999; 99US-0118902.
 PR 20-DEC-1999; 99US-0172754.
 XX
 PA (MERI) MERCK & CO INC.
 XX
 PI Bai C;
 XX
 DR WPI; 2000-506066/45.
 DR P-PSDB; AAY97246.
 XX
 PT Isolated human M68 nucleic acids and proteins which are part of the
 PT tumor necrosis factor receptor (TNFR) family, useful for identifying
 PT modulators that may be used to treat various diseases e.g. cancer,
 PT osteoporosis, Alzheimer's disease
 XX
 PS Claim 21; Page 73-75; 80pp; English.
 XX
 CC The M68 protein is a member of a family of proteins which have
 CC roles in immune responses, cell death, cell proliferation and
 CC stimulation of cell differentiation. M68 lacks a transmembrane domain
 CC and is a secreted factor suggesting that it functions as a natural
 CC inhibitor for its ligand. The altered expression pattern of M68 in a
 CC multitude of tissues suggests that M68 may play a role in cancer by
 CC binding to its ligand and blocking apoptotic cell death induced by
 CC such a ligand. This anti-apoptotic role of M68 suggests that
 CC modulators of M68 will be useful in treatment of apoptosis-related
 CC diseases such as various forms of cancer and various bone disorders.
 CC M68 nucleic acids and proteins are therefore useful for treating
 CC conditions involving atypical apoptosis and for identifying
 CC modulators of M68. Modulators of M68 are useful for treatment of
 CC cancer and other diseases associated with abnormal levels of

CC apoptosis including systemic lupus erythematosus, Hashimoto's
 CC thyroiditis, Grave's disease, idiopathic myxedema, autoimmune
 CC diabetes, thrombotic thrombocytopenic purpura, multiple sclerosis,
 CC liver diseases, autoimmune gastritis, ulcerative colitis,
 CC glomerulonephritis, pulmonary fibrosis, heart failure,
 CC atherosclerosis, aplastic anaemia, myelodysplastic syndromes,
 CC osteoporosis, Alzheimer's disease, Parkinson's disease, stroke, and
 CC myocardial infarction.

XX
 XX Sequence 1066 BP; 178 A; 367 C; 335 G; 186 T; 0 other;

Alignment Scores:
 Pred. No.: 4.59e-77 Length: 1066
 Score: 1491.00 Matches: 271
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 21 Gaps: 0

US-09-936-024-1 (1-271) x AAAS3802 (1-1066)

Qy 1 ValAlaGluThrProThrTyrProTrpArgAspAlaGluThrGlyValArgLeuValCys 20
 Db 140 GTGGCAGAAACACCACTACCCCTGGGGAGACGAGACAGAGCGGCTGTGTGC 199

Qy 21 AlaGlnCysProProGlyYThrPheValGlnArgProCysArgAspSerProThrThr 40
 Db 200 GCCCAGTGCCCGCCAGGACCTTTGTGAGCGCGCTGCCCGCCAGACGCCACGACG 259

Qy 41 CysGlyProCysProProAlaGlnHisTyrThrGlnPheTrpAsnTyrLeuGluArgCysArg 60
 Db 260 TGTGGCCCTGTCCACCGCGCCACTACACGAGTTCGAACTCTGAGACGCTGCGCGC 319

Qy 61 TyrCysAsnValLeuCysGlyValArgGluGluGlnAlaArgAlaCysHisAlaThrHis 80
 Db 320 TACTGCAACGCTCTGTGGGAGCGTGAGAGAGAGAGCGGCTTGCCACAGCCACCCAC 379

Qy 81 AsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHis 100
 Db 380 AACGTCCTGCGCTGCCCGCCAGCGGCTCTTCCGACACCTGTGTTGTGGAGCAC 439

Qy 101 AlaSerCysProProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGln 120
 Db 440 GCATCGTGTCCACTGGTGTGCGGCGGTATTGCCCGGACACCCCGACAGAACACGCGAG 499

Qy 121 CysGlnProCysProProGlyYThrPheSerAlaSerSerSerSerSerGluGlnCysGln 140
 Db 500 TGCACGCGTGTCCCGCCAGGACCTTCTCACGACGAGCTTCACGACGACGAGCTGCGAG 559

Qy 141 ProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerSerHis 160
 Db 560 CCCACCGCAACTCAGCGGCTGTGGGCTGACCTCAATGTGCCAGGCTCTTCTCCCAT 619

Qy 161 AspThrLeuCysThrSerCysThrGlyPheProLeuSerThrArgValProGlyAlaGlu 180
 Db 620 GACACCTGTGCAACCACTGCACTGGCTTCCCTCAGACACAGAGTACAGAGCTGAG 679

Qy 181 GluCysGluArgAlaValIleAspPheValAlaPheGlnAspIleSerIleValArgLeu 200
 Db 680 GAGGTAGGCTGCGTGCATGTGCTTGTGCTTCCAGGACATCTCCATCAAGGCTG 739

Qy 201 GlnArgLeuGlnAlaLeuGlnAlaProGlyGlyTyrGlyProThrProArgAlaGly 220
 Db 740 CAGCGGCTGTGCGAGGCTCTGAGGCGCCCGAGGCTGCGGTCCGACACCAAGGCGGCG 799

Qy 221 ArgAlaAlaLeuGlnLeuValLeuArgArgArgLeuThrGluLeuGlyAlaGlnAsp 240
 Db 800 CGCGCGGCTTGTGAGCTGAGCTGCTGTGCGGCTCAGGAGCTCTGTGGGCGCCAGAGAC 859

Qy 241 GlnAlaLeuLeuValArgLeuLeuGlnAlaLeuArgValAlaArgMetProGlyLeuGlu 260
 Db 860 GGGCGCTGTGTGTGCGGCTGTGCAAGCGCTGCGCGTGTGCGCAGAGATGCCGGGCTGAG 919

Qy 261 ArgSerValArgGluArgPheLeuProValHis 271
 Db 920 CGAGCGCTCGGTAGCGCTTCTCTCCCTGTGCAC 952

RESULT 14
 AAV39085
 ID AAV39085 standard; cDNA; 1077 BP.
 XX
 AC AAV39085;
 XX
 DT 26-OCT-1998 (first entry)
 XX
 DE Human tumour necrosis factor receptor-6 alpha cDNA.
 XX
 KW Human tumour necrosis factor receptor-6 alpha; TNFR-6 alpha; TNFR-6 beta;
 KW endothelial cells; keratinocytes; normal prostate; apoptosis;
 KW prostate tumour tissue; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 25..927
 FT /*tag= a
 FT /product= "TNFR-6 alpha protein"
 FT sig_peptide 25..114
 FT /*tag= b
 FT mat_peptide 115..924
 FT /*tag= c

PN WO9830694-A2.
 PD 16-JUL-1998.
 XX
 PF 13-JAN-1998; 98WO-US00153.
 XX
 PR 14-JAN-1997; 97US-0035496.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Ehner R, Feng P, Gentz RL, Ni J, Ruben SM, Yu G;
 XX
 DR WPI; 1998-399142/34.
 DR P-PSDB; AAW63622.
 XX
 PT Human tumour necrosis factor receptors 6-alpha and 6-beta - used in
 PT the diagnosis of immune system-related disorder(s)
 XX
 PS Disclosure; Fig 1; 91pp; English.
 XX

CC The present sequence represents the human tumour necrosis factor
 CC receptor-6 alpha (TNFR-6 alpha) cDNA. The invention also provides
 CC for the TNFR-6 beta cDNA (AAV39086). TNFR-6 alpha and TNFR-6 beta are
 CC members of the tumour necrosis factor receptor (TNFR) family. TNFRs
 CC are expressed in endothelial cells, keratinocytes, normal prostate and
 CC prostate tumour tissue. For a number of disorders of these cells,
 CC particularly of the immune system, substantially altered (whether
 CC increased or decreased) levels of TNFR-6 alpha and/or TNFR-6 beta gene
 CC expression can be detected, therefore the TNFR-6 alpha and TNFR-6 beta
 CC polypeptides, nucleic acids and antibodies are claimed to be useful in
 CC the diagnosis of such disorders. Mutations of the TNFR-6 alpha and
 CC TNFR-6 beta genes can also be detected. The TNFR polypeptides are
 CC also claimed to be useful for identifying ligands which may be useful
 CC in the treatment of apoptosis related disorders.

XX
 SQ Sequence 1077 BP; 196 A; 360 C; 326 G; 195 T; 0 other;

Alignment Scores:
 Pred. No.: 4.64e-77 Length: 1077
 Score: 1491.00 Matches: 271
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 19 Gaps: 0

US-09-936-024-1 (1-271) x AAV39085 (1-1077)

Qy 1 ValAlaGluThrProThyProTrpArgAspAlaGluThrGlyGluArgLeuValCys 20
Db 112 GTGGCAGAACACCCACCTTGTGCACGCGCGTGGCGCGAGACAGCGGCGCTGGTGTGC 171

Qy 21 AlaGlnCysProGlyThrPheValGlnArgProCysArgAspSerProThrThr 40
Db 172 GCCCAGTGCCTCCCGCAGCACCTTGTGCACGCGCGTGGCGCGAGACAGCGCCACGAGC 231

Qy 41 CysGlyProCysProArgHisTyThrGlnPheTrpAsnTyThrGluArgCysArg 60
Db 232 TGTGGCGCGTGTCCACGCGGCCACTACACGAGTTCTTGGAACTTACCTGGAGCGCTCCGC 291

Qy 61 TyCysAsnValLeuCysGlyGluArgGluGluAlaArgAlaCysHisAlaThrHis 80
Db 292 TACTGCAACGTCTCTGGGGGAGCGTGAGGAGGAGCAGCGGCTTGGCCAGCCACCCAC 351

Qy 81 AsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHis 100
Db 352 AACCGTGCCTCCCGCAGCACCGGCTTCTTCGCGCAGCGCTGGTTCTTGTGGAGCAC 411

Qy 101 AlaSerCysProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGln 120
Db 412 GCATCGTGTCCACCTGGTGCCTGGCGCGTGATTGCCCCGGGACACCCCGAGCAACGCGAG 471

Qy 121 CysGlnProCysProGlyThrPheSerAlaSerSerSerSerGluGlnCysGln 140
Db 472 TGCACGCGTGCCTCCCGCAGCACCTTCTCAGCCAGCAGCTCCAGCTCAGACGAGTGCAG 531

Qy 141 ProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerHis 160
Db 532 CCCACCGCAACTGCACGCGCCTGGGCGCTGGCCCTCAATGTGCAGGCTCTTCTCCCAT 591

Qy 161 AspThrLeuCysThrSerCysThrGlyPheProLeuSerThrArgValProGlyAlaGlu 180
Db 592 GACACCTGTGCACCACTGCATCGGCTTCCCGCTCAGCACCGGCTACCGAGGCTGAG 651

Qy 181 GluCysGluArgAlaValIleAspPheValAlaPheGlnAspIleLysArgLeu 200
Db 652 GAGTGTGAGGCTGCGCTCATCGACTTGTGGCTTTCAGGACATCTCCATCAGAGGCTG 711

Qy 201 GlnArgLeuLeuGlnAlaLeuGluAlaProGluGlyTrpGlyProThrProArgAlaGly 220
Db 712 CAGCGGCTGTGCAGGCGCTCGAGGCGCCCGAGGCGTGGGGTCCGACACCAAGGCGGGC 771

Qy 221 ArgAlaLeuGlnLeuLysLeuArgArgLeuThrGluLeuLeuGlyAlaGlnAsp 240
Db 772 CGCGCGGCTTGCAGCTGAAGCTGCGTGGCGGCTCAGCGAGCTCTCGGGGCGCAGGAC 831

Qy 241 GlyAlaLeuLeuValArgLeuLeuGlnAlaLeuArgValAlaArgMetProGlyLeuGlu 260
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Qy 261 ArgSerValArgGluArgPheLeuProValHis 271
Db 892 CGGAGCGTCCGTGAGCGCTTCTCCCTCGCTGTGCAC 924

RESULT 15

AAA37772
ID AAA37772 standard; DNA; 1077 BP.

XX

AC AAA37772;

XX

DT 04-DEC-2000 (first entry)

XX

DE Human tumour necrosis factor receptor-6 alpha coding sequence.

XX

KW Human; Tumour necrosis factor receptor 6; TNFR-6alpha; TNFR-6beta;
KW ocular neovascularisation; solid tumour; malignancy; prostate cancer;
KW breast cancer; colon cancer; diabetic retinopathy; microbial infection;
KW pre-maturity macular degeneration; allergy; inflammation; tissue damage;

```
Qy 21 AlagInCyseProProGlyThrPheValGlnArgProCysArgAaspSerProThrThr 40
Db 172 GCCAGTGCCTCCCGAGGACCTTTGTGAGCGGCGGTGCGCCGAGACAGCCCGACGACG 231
Qy 41 CyagIlyProCyseProProGlyHisTyrThrGlnPheTyrPheTyrLeuGlnArgCysArg 60
Db 232 TGTGGCCCGTGTCCACCGCGGCACTACACGCACTTCTGGAATCTACCTGAGCGGTGCGC 291
Qy 61 TyrCysAsnValLeuGlyGlyGlnArgGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 80
Db 292 TACTGCAAGCTCTCTGTGAGGAGCGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 351
Qy 81 AsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysAlaLeuGlnHis 100
Db 352 AACCGTGCCTGCGCGGCGGACCGGCTTCTTGGGACGCGTGTGTTCTGTGAGAGCAC 411
Qy 101 AlaseCyseProProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGln 120
Db 412 GCATCGTGTCCACCTGGTGTGCGGCGTGTATGCCCCGCGCACCCCGACGACAGACAGCAG 471
Qy 121 CysGlnProCyseProProGlyThrPheSerAlaSerSerSerSerSerSerSerSerSer 140
Db 472 TGCCAGCCGTGCCCCCGAGGACCTTCTCAGCCAGCAGCTCAGCTCAGCAGCTGCGAG 531
Qy 141 ProHisArgAsnCyseThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerSerHis 160
Db 532 CCCACCGCAACTGCAAGGCGCTGGGCGTGGCCCTCAATGTGCCAGGCTTCTCCCAT 591
Qy 161 AspThrLeuCyseThrSerCyseThrGlyPheProLeuSerThrArgValProGlyAlaGln 180
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Qy 181 GlucYsgIuArgAlaValIleAspPheValAlaPheGlnAspIleSerIleValArgLeu 200
Db 652 GAGTGTAGCGTGTGCTGTATGACTTTGTGCTTCCAGACATCTCCATCAAGAGGCTG 711
Qy 201 GlnArgLeuLeuGlnAlaLeuGlnAlaProGlnGlyTyrGlyProThrProArgAlaGly 220
Db 712 CAGCGGCTGTGCAAGGCGCTGAGGCGCCGAGGCGGTGGGTCGCGACACCAAGGCGGCGC 771
Qy 221 ArgAlaAlaLeuGlnLeuValLeuArgArgLeuThrGlnLeuLeuGlyAlaGlnAsp 240
Db 772 CGCGGCGCTTGTGAGCTGAGAGCTGTGCGGCGCTCAAGGAGCTCTGTGGGCGCAGGAC 831
Qy 241 GlyAlaLeuLeuValArgLeuLeuGlnAlaLeuArgValAlaArgMetProGlyLeuGln 260
Db 832 GGGCGGCTGTGTGTGCGCTGTGAGGCGCTGTGCGCGGTGCGCAGAGATGCCGAGCTGAG 891
Qy 261 ArgSerValArgGlnArgPheLeuProValHis 271
Db 892 CGGAGCGTCCCTGAGCGCTTCTCCTGTGTGAC 924
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Search completed: January 6, 2003, 11:31:11
Job time : 236 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 6, 2003, 11:15:32 ; Search time 21 Seconds
(without alignments)
535,242 Million cell updates/sec

Title: US-09-936-024-1

Perfect score: 1491
Sequence: 1 VAETPTYPWRDAETGERLVC.....RVARMGLERSYERELPVH 271

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match length	ID	Description
1	1491	100.0	300	TR6B_HUMAN	Q95407 homo sapien
2	440.5	29.5	401	TR1B_HUMAN	O00300 homo sapien
3	425.5	28.5	401	TR1B_RAT	O08727 rattus norv
4	424.5	28.5	401	TR1B_MOUSE	O08712 mus musculu
5	340.5	22.8	461	TR1B_HUMAN	P20333 homo sapien
6	332.5	22.3	474	TR1B_MOUSE	P25119 mus musculu
7	299.5	20.1	435	TRN3_HUMAN	P36941 homo sapien
8	288.5	19.3	655	TRN3_MOUSE	O9505 mus musculu
9	287	19.2	655	TR21_HUMAN	O75509 homo sapien
10	265.5	17.8	415	TRN3_MOUSE	P50284 mus musculu
11	260	17.4	349	CRMB_VARV	P34015 variola vir
12	257.5	17.3	349	CRMB_CAMPS	Q8UY47 camelpox vi
13	254.5	17.1	351	CRMB_COMPX	O73559 cowpox viru
14	244	16.4	283	TR1A_HUMAN	O92956 homo sapien
15	235.5	15.8	616	TR1I_HUMAN	O9Y666 homo sapien
16	234.5	15.7	325	VT2_SPKVA	P25943 shope fibro
17	220.5	14.8	625	TRN1_MOUSE	O35305 mus musculu
18	215.5	14.5	277	TRN4_HUMAN	P43469 homo sapien
19	211.5	14.2	277	TRN4_RAT	P15755 rattus norv
20	211	14.2	277	TRN5_HUMAN	P25942 homo sapien
21	210.5	14.1	326	VT2_MYXVL	P29825 myxoma viru
22	203	13.6	289	TRN5_MOUSE	P27512 mus musculu
23	202	13.5	269	TRN5_BOVIN	Q28203 bos taurus
24	194.5	13.0	272	TRN4_MOUSE	P47741 mus musculu
25	185	12.4	256	TRN3_MOUSE	P20334 mus musculu
26	182	12.2	535	TRN8_HUMAN	P28908 homo sapien
27	174	11.7	456	TRN9_HUMAN	O07011 homo sapien
28	171.5	11.5	416	TR16_CHICK	P18519 gallus gall
29	171	11.5	180	TR22_MOUSE	O9462 mus musculu
30	168	11.3	425	TR16_RAT	P07176 rattus norv
31	163	10.9	332	TRN6_PIG	O77736 sus scrofa
32	162	10.9	417	TR16_MOUSE	O92041 mus musculu
33	158	10.6	427	TR16_HUMAN	P08138 homo sapien

34	155.5	10.4	327	1	TRN6_MOUSE	P25446 mus musculu
35	155	10.4	323	1	TRN6_BOVIN	P51867 bos taurus
36	153	10.3	241	1	TR18_HUMAN	O9Y505 homo sapien
37	152.5	10.2	430	1	TR1T_MACFA	O9092 macaca fasc
38	151.5	10.2	430	1	TR1T_HUMAN	O96924 mus sapien
39	148.5	10.0	176	1	TR23_MOUSE	O9463 mus musculu
40	148	9.9	250	1	TRN7_MOUSE	P41272 mus musculu
41	147.5	9.9	5376	1	ZAN_MOUSE	O88799 mus musculu
42	145	9.7	335	1	TRN6_HUMAN	P25445 homo sapien
43	143.5	9.6	471	1	TR1A_BOVIN	O19131 bos taurus
44	142.5	9.6	260	1	TRN7_HUMAN	P26842 homo sapien
45	137.5	9.2	324	1	TRN6_RAT	Q63199 rattus norv

ALIGNMENTS

RESULT 1
TR6B_HUMAN STANDARD; PRT; 300 AA.
ID TR6B_HUMAN
AC Q95407;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE Tumor necrosis factor receptor superfamily member 6B precursor (Decoy receptor for Fas ligand) (Decoy receptor 3) (DCR3) (M6B).
GN TNFRSF6B OR DCR3 OR TR6.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI Taxid=9606;
RX MEDLINE=9067326; PubMed=9872321;
RA Pitti R.M., Marsters S.A., Lawrence D.A., Roy M., Kischkel F.C., Dowd P., Huang A., Donahue C.J., Sherwood S.W., Baldwin D.T., Goddard P.J., Wood W.I., Gurney A.L., Hillan K.J., Cohen R.L., Goddard A.D., Botstein D., Ashkenazi A.;
RT "genomic amplification of a decoy receptor for Fas ligand in lung and colon cancer.";
RL Nature 396:699-703 (1998).
RN [2]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 30-35.
RC TISSUE=Prostate;
RX MEDLINE=99253915; PubMed=10318773;
RA Yu K.-Y., Kwon B., Ni J., Zhai Y., Ebner R., Kwon B.S.;
RT "A newly identified member of tumor necrosis factor receptor superfamily (TR6) suppresses LIGHT-mediated apoptosis.";
RL J. Biol. Chem. 274:13733-13736 (1999).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=20122600; PubMed=10655513;
RA Bai C., Connolly B., Metzger M.L., Hilliard C.A., Liu X., Sandig V., Soderman A., Gallows S.M., Liu Q., Austin C.P., Caskey C.T.;
RT "Overexpression of M6B/DCR3 in human gastrointestinal tract tumors independent of gene amplification and its location in a four-gene cluster.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:1230-1235 (2000).
RN [4]
RP SEQUENCE FROM N.A.
RA Matthews L.;
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Decoy receptor for the cytotoxic ligands TNFSF4/LIGHT and TNFSF6/FasL. Protects against apoptosis.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Detected in fetal lung, brain and liver.

CC Detected in adult stomach, spinal cord, lymph node, trachea,
CC spleen, colon and lung. Highly expressed in several primary tumors
CC from colon, stomach, rectum, esophagus and in SW480 colon
CC carcinoma cells.
CC -1- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC -----
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CC -----
CC EMBL; AF104419; AAD03056.1; -
CC EMBL; AF134240; AAD29688.1; -
CC EMBL; AF217796; AAF35244.1; -
CC EMBL; AF217793; AAF33685.1; -
CC EMBL; AF217794; AAF33686.1; -
CC EMBL; AL121845; AAC03668.1; -
CC EMBL; BC017065; AAH17065.1; -
CC Genew; HGNC:11921; TNFRSF6B.
CC MIM; 603361; -
CC HSSP; O14763; 1D0G.
CC InterPro; IPR001368; TNFR_C6.
CC Pfam; PF00020; TNFR_C6; 4.
CC ProDom; PD000771; TNFR_C6; 1.
CC SMART; SM00208; TNFR_3.
CC PROSITE; PS00652; TNFR_NGFR_1; 2.
CC PROSITE; PS00050; TNFR_NGFR_2; 2.
KW Receptor; Apoptosis; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 29
FT CHAIN 30 300 TUMOR NECROSIS FACTOR RECEPTOR
FT
FT REPEAT 31 70
FT REPEAT 72 113 TNFR-CYS 1.
FT REPEAT 115 150 TNFR-CYS 2.
FT REPEAT 152 193 TNFR-CYS 3.
FT DISULFID 49 62 BY SIMILARITY.
FT DISULFID 52 70 BY SIMILARITY.
FT DISULFID 73 88 BY SIMILARITY.
FT DISULFID 91 105 BY SIMILARITY.
FT DISULFID 115 126 BY SIMILARITY.
FT DISULFID 132 150 BY SIMILARITY.
FT DISULFID 153 168 BY SIMILARITY.
FT DISULFID 174 193 BY SIMILARITY.
FT CARBOHYD 173 173 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 300 AA; 32679 MW; F90AEE33718449AF CRC64;
Query Match 100.0%; Score 1491; DB 1; Length 300;
Best Local Similarity 100.0%; Pred. No. 1.1e-110;
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VAETPTYPWDAETGERLVCAQCPGTFVORPCRRDPTTCGCPPHYTFQWNYLERCR 60
DB 30 VAETPTYPWDAETGERLVCAQCPGTFVORPCRRDPTTCGCPPHYTFQWNYLERCR 89
QY 61 YCNVLGCEEREERARACHATNRCRCRTGFFAHAGFCLHASCPGAGVIAPGTPSQNTQ 120
DB 90 YCNVLGCEEREERARACHATNRCRCRTGFFAHAGFCLHASCPGAGVIAPGTPSQNTQ 149
QY 121 CQCPGPTFGASSSSSSQCPHRCNTALGLALNVPSSSHDTTCTCTGTPPLSTRVPGAE 180
DB 150 CQCPGPTFGASSSSSSQCPHRCNTALGLALNVPSSSHDTTCTCTGTPPLSTRVPGAE 209
QY 181 ECERAVIDFAFODISTKRLQRLQALEAPEGWGPTRAGRAALQKLRRLTELLGAQD 240
DB 210 ECERAVIDFAFODISTKRLQRLQALEAPEGWGPTRAGRAALQKLRRLTELLGAQD 269
QY 241 GALLVRLQLQALRVARMPGLERSVRERFLPVH 271
DB 270 GALLVRLQLQALRVARMPGLERSVRERFLPVH 300

RESULT 2
T11B_HUMAN
ID T11B_HUMAN STANDARD; PRT; 401 AA.
AC O00300; O60236; Q9UHP4;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 11B precursor
DE (Osteoprotegerin) (Osteoclastogenesis inhibitory factor).
GN TNFRSF11B OR OPG OR OCIF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
SE SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=97262071; PubMed=9108485;
RA Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,
RA Luethy R., Nguyen H.Q., Woodson S., Bennett L., Boone T., Shimamoto G.,
RA Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,
RA Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,
RA Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,
RA Suggs S., Boyle W.J.;
RA "Osteoprotegerin: a novel secreted protein involved in the regulation
RT of bone density.";
RL Cell 89:309-319(1997).
RN (2)
RP SEQUENCE FROM N.A.
RC TISSUE=Lung cancer;
RX MEDLINE=98151033; PubMed=9492069;
RA Yasuda H., Shima N., Nakagawa N., Mochizuki S.-I., Yano K., Fujise N.,
RA Sato Y., Goto M., Yamaguchi K., Kuriyama M., Kanno T., Murakami A.,
RA Tsuda E., Morinaga T., Higashio K.;
RT "Identity of osteoclastogenesis inhibitory factor (OCIF) and
RT osteoprotegerin (OPG): a mechanism by which OPG/OCIF inhibits
RL osteoclastogenesis in vitro.";
RL Endocrinology 139:1329-1337(1998).
RN (3)
RP SEQUENCE FROM N.A., AND VARIANT ASN-3.
RC TISSUE=Placenta;
RX MEDLINE=98351569; PubMed=9688283;
RA Morinaga T., Nakagawa N., Yasuda H., Tsuda E., Higashio K.;
RT "Cloning and characterization of the gene encoding human
RT osteoprotegerin/osteoclastogenesis-inhibitory factor.";
RL Eur. J. Biochem. 254:685-691(1998).
RN (4)
RP SEQUENCE FROM N.A., AND VARIANT ASN-3.
RC TISSUE=Eye;
RA Strausberg R.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
RN (5)
RP SEQUENCE OF 22-36 AND 378-401.
RX MEDLINE=98238445; PubMed=9571159;
RA Tomoyasu A., Goto M., Fujise N., Mochizuki S.-I., Yasuda H.,
RA Morinaga T., Tsuda E., Higashio K.;
RT "Characterization of monomeric and homodimeric forms of
RT osteoclastogenesis inhibitory factor.";
RL Biochem. Biophys. Res. Commun. 245:382-387(1998).
RN (6)
RP SEQUENCE OF 22-393 FROM N.A.
RC TISSUE=Placenta;
RA He Z.-Y., Yang G.-Z., Zhang W.-J., Wu X.-F.;
RT "Cloning and expression of osteoprotegerin from Homo sapiens.";
RL Acta Biochim. Biophys. Sin. 31:680-684(1999).
RN (7)
RP SEQUENCE OF 242-255; 354-359 AND 369-378, AND FUNCTION.
RX MEDLINE=97312536; PubMed=9168977;
RA Tsuda E., Goto M., Mochizuki S.-I., Yano K., Kobayashi F.,
RA Morinaga T., Higashio K.;
RT "Isolation of a novel cytokine from human fibroblasts that

RT specifically inhibits osteoclastogenesis.";
 RL Biochem. Biophys. Res. Commun. 234:137-142(1997).
 RN [8]
 RP TRAIL BINDING.
 RX MEDLINE=98269100; PubMed=9603945;
 RA Emery J.G., McDonnell P., Burke M.B., Deen K.C., Lyn S., Silverman C.,
 RA Dul E., Appelbaum E.R., Bichman C., DiPrinzio R., Dadds R.A.,
 RA James I.E., Rosenberg M., Lee J.C., Young P.R.;
 RT Osteoprotegerin is a receptor for the cytotoxic ligand TRAIL.";
 RL J. Biol. Chem. 273:14363-14367(1998).
 RN [9]
 RP CHARACTERIZATION, AND MUTAGENESIS OF CYS-400.
 RX MEDLINE=98148058; PubMed=9478964;
 RA Yamaguchi K., Kinoshita K., Goto M., Kobayashi F., Tsuda E.,
 RA Morinaga T., Higashio K.;
 RT Characterization of structural domains of human osteoclastogenesis
 RT inhibitory factor.";
 RL J. Biol. Chem. 273:5117-5123(1998).
 RN [10]
 RP REVIEW.
 RX MEDLINE=21395914; PubMed=11505389;
 RA Hofbauer L.C., Neuber A., Heufelder A.E.;
 RT Receptor activator of nuclear factor-kappaB ligand and
 RT osteoprotegerin: potential implications for the pathogenesis and
 RT treatment of malignant bone diseases.";
 RL Cancer 92:460-470(2001).
 CC -1- FUNCTION: Acts as decoy receptor for RANKL and thereby neutralizes
 CC its function in osteoclastogenesis. Inhibits the activation of
 CC osteoclasts and promotes osteoclast apoptosis in vitro. Bone
 CC homeostasis seems to depend on the local RANKL/OPG ratio. May also
 CC play a role in preventing arterial calcification. May act as decoy
 CC receptor for TRAIL and protect against apoptosis. TRAIL binding
 CC blocks the inhibition of osteoclastogenesis.
 CC -1- SUBUNIT: Homodimer.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Highly expressed in adult lung, heart, kidney,
 CC liver, spleen, thymus, prostate, ovary, small intestine, thyroid,
 CC lymph node, trachea, adrenal gland, testis, and bone marrow.
 CC Detected at very low levels in brain, placenta and skeletal
 CC muscle. Highly expressed in fetal kidney, liver and lung.
 CC -1- INDUCTION: Upregulated by increasing calcium concentration in the
 CC medium and estrogens. Downregulated by glucocorticoids.
 CC -1- PAM: N-glycosylated. Contains acidic acid residues.
 CC -1- PAM: N-terminus may be blocked.
 CC -1- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
 CC -1- SIMILARITY: CONTAINS 2 DEATH DOMAINS.
 CC -1- SIMILARITY: CONTAINS 2 DEATH DOMAINS.
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KW Receptor; Apoptosis; Glycoprotein; Repeat; Signal; Polymorphism.
 FT SIGNAL 1 21
 FT CHAIN 22 401
 FT
 FT REPEAT 24 62
 FT REPEAT 65 105
 FT REPEAT 107 142
 FT REPEAT 145 185
 FT REPEAT 198 269
 FT DOMAIN 270 365
 FT SITE 400 400
 FT DISULFID 41 54
 FT DISULFID 44 62
 FT DISULFID 65 97
 FT DISULFID 83 97
 FT DISULFID 87 105
 FT DISULFID 107 118
 FT DISULFID 124 142
 FT DISULFID 145 160
 FT DISULFID 166 185
 FT CARBOHYD 152 152
 FT CARBOHYD 165 165
 FT CARBOHYD 178 178
 FT CARBOHYD 289 289
 FT VARIANT 3 3
 FT MUTAGEN 400 400
 FT MUTAGEN 400 401
 FT CONFLICT 263 263
 SQ SEQUENCE 401 AA; 46040 MW; EDFA48B67D86C71E CRC64;
 Query Match 29.5%; Score 440.5; DB 1; Length 401;
 Best Local Similarity 41.2%; Pred. No. 8.7e-28;
 Matches 77; Conservative 31; Mismatches 74; Indels 5; Gaps 2;
 QY 5 PTYPWRDAETGERLVACQCPGTFVQRCRRDSPTTCGPPRRHYTOFMWYLERCRYCNV 64
 Db PKVHYHVEBHSHTOLCKCPGTLKQHTAKMTVCAPCDHYTDSMTSDCLCSP 85
 QY 65 LGRREBEADACATNTRACRCRTGFPAAHAGFCLEHASCPPGACVIAPIGPSNTQCOPC 124
 Db VCKELQYVKQECNTRHNRVCEKGRYLEIEFLKHSRCPGFGVQAGPERRVTCKRC 145
 QY 125 PPGTFSSSSSSSECCQHRNCTALGLANVPSSSHTLTCTSCGFPLSTRVGAEE-C 182
 Db 146 PDGFSNETSKAPCRKHTNCSVFGILLTKGATHDNI---CSGNSSTQCGIDVTL 202
 QY 183 ERAVIDF 189
 Db 203 EAERFR 209
 RESULT 3
 T11B RAT STANDARD; PRT; 401 AA.
 ID T11B RAT
 AC 00872;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 11B precursor
 DE (osteoprotegerin).
 DE TNFRSF11B OR OPG.
 GN Rattus norvegicus (Rat).
 OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_Taxid=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryonic Intestine;
 RX MEDLINE=97262071; PubMed=9108485;
 RA Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,
 RA Luehly R., Nguyen H.O., Wooden S., Bennett L., Boone T., Shimamoto G.,

CC whereas expression decreases at day 11 and increases from day 15
 CC to 17. On day 15 found in developing bone primordia,
 CC brachiocephalic artery and ductus arteriosus, left main bronchus,
 CC abdominal aorta and midgut.
 CC -1- INDUCTION: Upregulated by TGF-beta and estrogens. Downregulated by
 CC 1,25-dihydroxyvitamin D3 and parathyroid hormone.
 CC -1- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
 CC -1- SIMILARITY: CONTAINS 2 DEATH DOMAINS.
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; U94331; AAB53708.1; -.
 DR EMBL; AB013898; BAA28269.1; -.
 DR EMBL; AB013903; BAA33388.1; -.
 DR EMBL; AB013899; BAA33388.1; JOINED.
 DR EMBL; AB013900; BAA33388.1; JOINED.
 DR EMBL; AB013901; BAA33388.1; JOINED.
 DR EMBL; AB013902; BAA33388.1; JOINED.
 DR HSSP; P25942; 1CDF.
 DR MGD; MGI:109587; Tnfra511b.
 DR InterPro; IPR000488; Death.
 DR InterPro; IPR001368; TNFR_c6.
 DR Pfam; PF00020; TNFR_c6; 3.
 DR ProDom; PD000771; TNFR_c6; 1.
 DR SMART; SM00005; DEATH; 1.
 DR SMART; SM00208; TNFR; 4.
 DR PROSITE; PS50017; DEATH DOMAIN; 1.
 DR PROSITE; PS00652; TNFR_NGFR_2; 2.
 DR PROSITE; PS50050; TNFR_NGFR_2; 2.
 DR Receptor; Apoptosis; Glycoprotein; Repeat; Signal; Polymorphism.
 KW CHAIN 1 21
 FT SIGNAL 1 21
 FT CHAIN 22 401
 FT REPEAT 24 62
 FT REPEAT 65 105
 FT REPEAT 107 142
 FT REPEAT 145 185
 FT DOMAIN 198 269
 FT DOMAIN 283 365
 FT SITE 400 400
 FT DISULFID 41 54
 FT DISULFID 44 62
 FT DISULFID 65 80
 FT DISULFID 83 97
 FT DISULFID 107 118
 FT DISULFID 124 142
 FT DISULFID 145 160
 FT DISULFID 166 185
 FT CARBOHYD 98 165
 FT CARBOHYD 178 178
 FT CARBOHYD 289 289
 FT VARIANT 138 138
 FT VARIANT 161 161
 FT VARIANT 165 165
 FT VARIANT 288 288
 FT VARIANT 296 296
 FT SEQUENCE 401 AA; 45923 MM; CAA610203B312470 CRC64;
 Query Match 28.5%; Score 424.5; DB 1; Length 401;
 Best Local Similarity 39.0%; Pred. No. 1.6e-26;

Matches 80; Conservative 32; Mismatches 88; Indels 5; Gaps 2;
 QY 5 PTYPMDAERGERLVAQCPPTGFVORPCGRDPTTCGCPPEPHYTFQWMLYRCRYCNV 64
 DB 26 PKLIHDPERTGHOILCDKAPGYLKHCHTVRKRTLCVPEPDHSYDSWHTSDECYCSP 85
 QY 65 LCGEREERARACHATNHRACRCRTGFPFMAAGFCLERASCPGAGVIAPTGSPONTQCP 124
 DB 86 VKELQSVKQECNRTNHRVCECEGRYLEIEFLKHSRCPGSGVQAGTPERNVCKKC 145
 QY 125 PPGTFSSSSSSQCCPHRCTALGLANVPGSSSDTLCTGTFPLSTRVGAEE--C 162
 DB 146 PDGFSEETSKAPCLKHNCSTFFGLLLQKGNATHDV--CSGNREATQKGIQVTL 202
 QY 183 ERAVIDFAFQDISIKRLQRLQAL 207
 DB 203 EBAFFRAVPTKLIIPMWLSVVDL 227
 RESULT 5
 ID TRIB HUMAN STANDARD; PRT; 461 AA.
 AC P20333; Q16042;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 1B precursor (Tumor
 DE necrosis factor receptor 2) (p80) (TNF-R2) (p75) (CD120b) (Ectanecept)
 DE [contains: Tumor necrosis factor binding protein 2 (TNFR2)]
 GN TNFRSF1B OR TNFR2 OR TNFR.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90260639; PubMed=2160731;
 RA Smith C.A., Davis T., Anderson D., Solam L., Beckmann M.P., Jerzy R.,
 RA Dower S.K., Cosman D., Goodwin R.G.;
 RT "A receptor for tumor necrosis factor defines an unusual family of
 RT cellular and viral proteins.";
 RL Science 248:1019-1023(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91045991; PubMed=2172983;
 RA Kohno T., Brewer M.T., Baker S.L., Schwartz P.E., King M.W.,
 RA Hale K.K., Squires C.H., Thompson R.C., Vannice J.L.;
 RT "A second tumor necrosis factor receptor gene product can shed a
 RT naturally occurring tumor necrosis factor inhibitor.";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:8331-8335(1990).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9629745; PubMed=8661109;
 RA Bellinger C.P., White P.S., Maris J.M., Sulman E.P., Jensen S.J.,
 RA Lepaelder D., Stallard B.J., Goeddel D.V., Desauvage F.J.;
 RA Brodeur G.M.;
 RT "Physical mapping and genomic structure of the human TNFR2 gene.";
 RL Genomics 35:94-100(1996).
 RN [4]
 RP SEQUENCE OF 37-461 FROM N.A.
 RX MEDLINE=91370690; PubMed=1966549;
 RA Dembic Z., Loetscher H., Gubler U., Pan Y.C., Lahm H.W., Gentz R.,
 RA Brockhaus M., Lesslauer W.;
 RT "Two human TNF receptors have similar extracellular, but distinct
 RT intracellular, domain sequences.";
 RL Cytokine 2:231-237(1990).
 RN [5]
 RP SEQUENCE OF 116-461 FROM N.A. AND PARTIAL SEQUENCE.
 RX MEDLINE=90349572; PubMed=2166946;
 RA Heller R.A., Song K., Onasch M.A., Fischer W.H., Chang D.,
 RA Ringold G.M.;
 RT "Complementary DNA cloning of a receptor for tumor necrosis factor
 RT and demonstration of a shed form of the receptor.";

RX MEDLINE-94225209; PubMed-8171323;
RA Crowe P.D., van Arsdale T.L., Walter B.N., Ware C.F., Hession C.,
RA Ehrenfelds B., Browning J.L., Din W.S., Goodwin R.G., Smith C.A.;
RT "A lymphotoxin-beta-specific receptor.";
RN Science 264:707-710(1994).
RL [4]
RP CHARACTERIZATION. PubMed-10207006;
RX MEDLINE-99223511; PubMed-10207006;
RA Wu M.-Y., Wang P.-Y., Han S.-H., Heieh S.-L.;
RT "The cytoplasmic domain of the lymphotoxin-beta receptor mediates cell
RT death in HeLa cells.";
RL J. Biol. Chem. 274:11868-11873(1999).
RP [5]
RP FUNCTION.
RX MEDLINE-20261554; PubMed-10799510;
RA Rooney I.A., Butrovich K.D., Glass A.A., Borboroglu S., Benedict C.A.,
RA Whitebeck J.C., Cohen G.H., Eisenberg R.J., Ware C.F.;
RT "The lymphotoxin-beta receptor is necessary and sufficient for
RT LIGHT-mediated apoptosis of tumor cells.";
RL J. Biol. Chem. 275:14307-14315(2000).
CC -1- FUNCTION: Receptor for the heterotrimeric lymphotoxin containing
CC LTA and LTB, and for TNFSF14/LIGHT. Promotes apoptosis via TRAF3
CC and TRAF5. May play a role in the development of lymphoid organs.
CC -1- SUBUNIT: Self-associates.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
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CC -----
DR ENBL; L04270; AAA36757.1; --
DR HMBL; BC026262; AAR26262.1; --
DR HSSP; P25942; ICDF.
DR Genew; HGNC:6718; LTBR.
DR MIM; 600979; --
DR InterPro; IPR001368; TNFR_C6.
DR Pfam; PF00020; TNFR_C6; 4.
DR ProDom; PD000771; TNFR_C6; 1.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS00500; TNFR_NGFR_2; 3.
KW Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
FT SIGNAL 1
FT CHAIN 31 435
FT TUMOR NECROSIS FACTOR RECEPTOR
FT SUPERFAMILY MEMBER 3.
FT DOMAIN 31 227
FT TRANSMEM 228 248
FT DOMAIN 249 435
FT CYTOPLASMIC (POTENTIAL).
FT REPEAT 42 81
FT REPEAT 82 124
FT REPEAT 125 168
FT REPEAT 169 211
FT DISULFID 43 58
FT DISULFID 59 72
FT DISULFID 62 80
FT DISULFID 83 98
FT DISULFID 101 116
FT DISULFID 104 124
FT DISULFID 126 132
FT DISULFID 139 148
FT DISULFID 142 167
FT DISULFID 170 185
FT CARBOHYD 40 40
FT CARBOHYD 177 177
SQ SEQUENCE 435 AA; 46709 MW; 624626E6022F656F CRC64;
Query Match 20.18; Score 299.5; DB 1; Length 435;
Best Local Similarity 32.0%; Pred. No. 1.2e-16;

Matches 74; Conservative 27; Mismatches 101; Indels 29; Gaps 9;
QY 13 ETGERLVACQPGTGVQPCRDSPPTTCGCPPEPRHYTQFWNYL----ERCRYCNVLCGER 69
DB 52 EPOHRICSCRCPPGTYSKACGRIRDTVCATCAENSYNHWNLYLTICQLCRPCDPVWG-- 109
QY 70 EEEARACHATHNRACRCRTGFFAHAGFCLE--H---ASCPGCA-GVIAPGTPSQNTQCQ 122
DB 110 LEEIAPCTSKRKTQCRQCPGMFC-AAWALECTHCELLSDCPGTEAEKDXKGVGNHCV 168
QY 123 PCPPGTFSSASSSEQCQPHRNCTALGLALNVPGSSSHDTLCTCTGTFPLSTRVPGABEC 182
DB 169 PCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAAQSDTCKNPLE-PLPPMSGTMLM 227
QY 183 ERAVIDFAVAFQDIS-----IKRLQLLOALEAPECGWGTTPRAG 220
DB 228 LAVLLPFAFLLATVFCSTWKSHPSLCRKLGSLK--RRPQEGNPNVAG 276
RESULT 8
TR21_MOUSE STANDARD; PRT; 655 AA.
ID TR21_MOUSE Q9EPUS; Q91XH9; Q91W77;
AC Q9EPUS; Q91XH9; Q91W77;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor receptor-6 (Death receptor 6).
DE related death receptor-6 (TNFRSF21 OR DR6).
GN TNFRSF21 OR DR6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Kidney;
RA Isogai D., Ichino M., Yoshinari M., Yamaura A., Kurokawa F.,
RA Minami M.;
RT "Mouse DR6: mouse homolog of human TNFR-related death receptor-6
RT (DR6).";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Kidney;
RA Kim V., Machleidt T., Shi W.-X., Wang X., Cai Z.;
RT "Murine DR6: murine TNFR-related death receptor-6.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP FUNCTION.
RX MEDLINE-21571606; PubMed-11714751;
RA Zhao H., Yan M., Wang H., Erickson S., Grewal I.S., Dixit V.M.;
RT "Impaired c-Jun amino terminal Kinase activity and T cell
RT differentiation in death receptor 6-deficient mice.";
RL J. Exp. Med. 194:1441-1448(2001).
CC -1- FUNCTION: May activate NF-kappa-B and promote apoptosis (By
CC similarity). May activate JNK and be involved in T-cell
CC differentiation.
CC -1- FUNCTION: May activate NF-kappa-B and JNK and promote apoptosis.
CC May be involved in T-cell differentiation.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Probable).
CC -1- TISSUE SPECIFICITY: Ubiquitous. Highly expressed in adult spleen,
CC thymus, testis, prostate, ovary, small intestine, colon, brain,
CC lung and kidney, and in fetal brain, liver and lung. Detected at
CC lower levels in adult peripheral blood leukocytes, lung, and in
CC fetal muscle, heart, kidney, small intestine and skin. Detected in
CC T-cells, B-cells and monocytes. In T-cells expression is highest
CC in Th0 cells, intermediate in Th2 cells and lower in Th1 cells.
CC -1- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.

Query Match	Similarity	Score	DB 1	Length	655
Best Local	Similarity	29.7%	Pred.	1.4e-15	
Matches	69	Conservative	32	Mismatches	116
				Indels	15
				Gaps	3
QY	6	TYPMWDAETGERLVCACGCPGTFVORPCRRDSPTTCGCPRRHYQFMWYLERCRYCNVL	65		
DB	53	TYRHVDRTTGGVLTCDCKPAGTYVSEHCTNMSLRVCCSSCPAGTFRRHENGIERCHDCSQP	112		
QY	66	CGEREERARACIATNRRACRCRTGFFALAGFLERLASCPRGAGVIAFGTPPSQNTCCQCP	125		
DB	113	CPWMEIERLPCALLDRECI CPPGMVQNSGTAPHTVCVGVGVKKGTENEDVACKOCA	172		
QY	126	PQTFASASSSSSEOCQPHNRCTALGALANVPGSSSHDTLCTGCGPL--STRVGAEC	182		
DB	173	RGTFSDVSSVWKKCAHHDCLGONLEVVAKPGIKETDNYC---GMRLPFSSSTNPFSSGIV	228		
QY	183	ERAVIDEVAFODISIKRLQRLQLALEAPRGWGPTRPAGRALQTLKRLRRLTE	234		

```

Db      229   TFSHPHSHSDVPSSTY-----PCGANSIDSNASTAVRTVPSCIE 272

RESULT 9
TR21_HUMAN
ID     TR21_HUMAN          STANDARD;             PRT;           655 AA.
AC      075509; Q96D86;
DT      15-JUN-2002 (Rel. 41, Created)
DT      15-JUN-2002 (Rel. 41, Last sequence update)
DT      15-JUN-2002 (Rel. 41, Last annotation update)
DE      Tumor necrosis factor receptor superfamily member 21 precursor (TNFR-
DE        related death receptor-6) (Death receptor 6).
CN      TNFRSF21 OR DR6.
OC      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxId=9606;
[1]
SEQUENCE FROM N.A.
RX      MEDLINE=98378343; PubMed=9714541;
RA      Pan G., Bauer J.H., Haridas V., Wang S., Liu D., Yu G., Vincenz C.,
RA      Aggarwal B.B., Ni J., Dixit V.M.;
RT      "Identification and functional characterization of DR6, a novel death
RT      domain-containing TNF receptor."
RL      FEBS Lett. 431:351-356(1998).
RN      RN
RP      SEQUENCE FROM N.A.
RA      Parker A.;
RL      Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
RN      RN
[3]
SEQUENCE FROM N.A.
RP      TISSUE=Brain, and Colon;
RA      Straubeberg R.;
RL      Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
CC      CC
[1]- FUNCTION: May activate NF-kappa-B and JNK and promote apoptosis.
[1]- SUBUNIT: Associates with TRADD.
[1]- SUBCELLULAR LOCATION: Type I membrane protein (Probable).
[1]- TISSUE SPECIFICITY: Highly expressed in heart, brain, placenta,
pancreas, lymph node, thymus and prostate. Detected at lower
levels in lung, skeletal muscle, kidney, testis, uterus, small
intestine, colon, spleen, bone marrow and fetal liver. Very low
levels were found in adult liver and peripheral blood leukocytes.
[1]- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
[1]- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
[1]- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-25 IS THE INITIATOR.
CC      CC
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```
FT SIGNAL 1 41 POTENTIAL
FT CHAIN 42 655 TUMOR NECROSIS FACTOR RECEPTOR
FT SUPERFAMILY MEMBER 21.
FT DOMAIN 42 349 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 350 370 POTENTIAL.
FT DOMAIN 371 655 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 415 498 DEATH.
FT REPEAT 50 88 TNFR-CYS 1.
FT REPEAT 90 131 TNFR-CYS 2.
FT REPEAT 133 167 TNFR-CYS 3.
FT REPEAT 170 211 TNFR-CYS 4.
FT DISULFID 67 80 BY SIMILARITY.
FT DISULFID 70 88 BY SIMILARITY.
FT DISULFID 91 106 BY SIMILARITY.
FT DISULFID 109 123 BY SIMILARITY.
FT DISULFID 113 131 BY SIMILARITY.
FT DISULFID 133 144 BY SIMILARITY.
FT DISULFID 150 168 BY SIMILARITY.
FT DISULFID 171 186 BY SIMILARITY.
FT DISULFID 192 211 BY SIMILARITY.
FT CARBOHYD 82 82 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 252 252 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 257 257 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 278 278 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT SSEQUENCE 655 AA; 71844 MW; 48939391C4852A33 CRC64;

Query Match 19.2%; Score 287; DB 1; Length 655;
Best Local Similarity 34.3%; Pred. No. 1.8e-15;
Matches 58; Conservative 23; Mismatches 88; Indels 0; Gaps 0;

QY 6 TYPRDRAETGERLVCAQCPGTFVQRPCCRDSPTTCGPPRHVYQFWNYLERCRYCNVL 65
Db 53 TYRHVDRATGOVLTCDCPKAGTVVSEHTNLSRVCSGCVGTFRHENGIEKCHDCSQP 112
QY 66 CGREEREARACHATHNACRCRTGFFAHAGFCLHASCPPGAGVIAPTGTSQNTQCP 125
Db 113 CPWPMIEKLPKCAALTDRECTCPGFMFOSNATCAPHTVCPGVGVRKKGTTEDVRCKQCA 172
QY 126 PGTFPSASSSSSEOCQPHRNCCTALGLALNVPGSSSHDTLCTCTGFFPLST 174
Db 173 RGTFSDVPSSVMKCKATYDCLSQLNLVVKPGTKETDNCVGLTSPFSST 221

RESULT 10
TNR3 MOUSE
ID TNR3 MOUSE STANDARD; PRT; 415 AA.
AC P50284;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 3 precursor
DE (lymphotoxin-beta receptor).
GN LTB or TNFRSF3 or TNFR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CVB; TISSUE=Lung;
RX MEDLINE=96072804; PubMed=7594541;
RA Force W.R., Walter B.N., Hession C., Tizard R., Kozak C.A.,
RA Browning J.L., Ware C.F.;
RT "Mouse lymphotoxin-beta receptor. Molecular genetics, ligand binding,
RT and expression.";
RL J. Immunol. 155:5280-5288 (1995).
RN [2]
RX SEQUENCE FROM N.A.
RX MEDLINE=96163885; PubMed=8586432;
RA Nakamura T., Tashiro K., Nazarea M., Nakano T., Sasayama S.,
RA Honjo T.;
```

```
RT RT "The murine lymphotoxin-beta receptor cDNA: isolation by the signal
RT sequence trap and chromosomal mapping.";
RL Genomics 30:312-319(1995).
CC -!- FUNCTION: Receptor for the heterotrimeric lymphotoxin containing
CC LTA and LTB, and for TNFSF14/LIGHT. Promotes apoptosis via TRAF3
CC and TRAF5. May play a role in the development of lymphoid organs
CC (By similarity)
CC -!- SUBUNIT: Self-associates (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC
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CC
CC EMBL; U29173; AAA68964.1; -
CC EMBL; U38423; AAB00846.1; -
CC EMBL; U30798; AAA81334.1; -
CC HSSP; O14763; IDOG.
CC MGD; MGI:104875; Ltbr.
CC InterPro; IPR001368; TNFR_C6.
CC Pfam; PF00020; TNFR_C6; 3.
CC ProDom; PD000771; TNFR_C6; 1.
CC SMART; SM00208; TNFR; 3.
CC
CC PROSITE; PS00652; TNFR_NGFR_1; 2.
CC PROSITE; PS00500; TNFR_NGFR_2; 3.
CC Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 30 POTENTIAL.
FT CHAIN 31 415 TUMOR NECROSIS FACTOR RECEPTOR
FT DOMAIN 31 223 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 224 244 SUPERFAMILY MEMBER 3.
FT DOMAIN 245 415 POTENTIAL.
FT REPEAT 42 81 CYTOPLASMIC (POTENTIAL).
FT REPEAT 82 124 TNFR-CYS 1.
FT REPEAT 125 170 TNFR-CYS 2.
FT REPEAT 171 213 TNFR-CYS 3.
FT DISULFID 43 58 BY SIMILARITY.
FT DISULFID 59 72 BY SIMILARITY.
FT DISULFID 62 80 BY SIMILARITY.
FT DISULFID 83 98 BY SIMILARITY.
FT DISULFID 101 116 BY SIMILARITY.
FT DISULFID 126 132 BY SIMILARITY.
FT DISULFID 139 150 BY SIMILARITY.
FT DISULFID 142 169 BY SIMILARITY.
FT DISULFID 172 187 BY SIMILARITY.
FT CARBOHYD 40 40 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 179 179 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT SSEQUENCE 415 AA; 44956 MW; 29B326A566AEF661 CRC64;

Query Match 17.8%; Score 265.5; DB 1; Length 415;
Best Local Similarity 30.9%; Pred. No. 5.6e-14;
Matches 72; Conservative 24; Mismatches 88; Indels 49; Gaps 10;

QY 20 CAQCPGTFVQRPCCRDSPTTCGPPRHVYQFWNYL---ERCRCYNVLCGEREEARAC 76
Db 59 CSRCPPGGEFVAVCSQDVTCKTCHNSYNHWNHLSQLCRPCDIVLG--FEVAPC 116
QY 77 HATHNACRCRTGFFAHAGFCL----EHASCPGAGVIA-PGTPSQNT-----QCQP 123
Db 117 TSDRKAECRCQGM-----SCVLDNECVHCEBERLVLCQGTAEVTDIMTDVNCVP 171
QY 124 CPPTGTSASSSSSEOCQPHRNCCTALGLALNVPGSSSHDILCTCTGFFPLSTRVPGAECE 183
Db 172 CKPGHFQNTSSPRARCOPHTRCBIQGLVEAAPGTSDTICK-----NPPEFGMLLL 224
QY 184 RAVIDFVAF-----QDISIKRLQRLQLALEAPEGMG-----PTPRA 219
```

Db 225 ALLSVLFTTTLACAMRHPSLCKRLTLK--RHPEGEESPCCAPRA 275

RESULT 11

CRMB_VARY STANDARD; PRT; 349 AA.

AC P34015; Q89098; Q85407; Q89118;

DT 01-FEB-1994 (Rel. 28, Created)

DT 01-FEB-1994 (Rel. 28, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Soluble TNF receptor II precursor (cytokine response modifying protein B).

GN CRMB OR G2R OR G4R.

OS Variola virus.

OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae; Orthopoxvirus.

OX NCBI_TaxID=10255;

RN (1)

RP SEQUENCE FROM N.A.

RC STRAIN=India-1967 / Isolate Ind;

RX MEDLINE=93202281; PubMed=8364129;

RA Shchelkunov S.N., Blinov V.M., Sandakhchiev L.S.;

RT "Genes of variola and vaccinia viruses necessary to overcome the host protective mechanisms.";

RL FEBS Lett. 319:80-83(1993).

RN (2)

RP SEQUENCE FROM N.A.

RC STRAIN=Bangladesh-1975;

RX MEDLINE=94088747; PubMed=8264798;

RA Masung R.F., Eposito J.J., Liu L., Qi J., Uteback T.R., Knight J.C., Audin L., Yuran T.E., Parsons J.M., Loparev V.N., Seliavanov N.A., Cavallaro K.F., Kerlavage A.R., Mahy B.W.J., Venter C.J.;

RT "Potential virulence determinants in terminal regions of variola smallpox virus genome.";

RL Nature 366:748-751(1993).

RN (3)

RP SEQUENCE FROM N.A.

RC STRAIN=Garcia-1966, and Somalia-1977;

RA Masung R.F., Loparev V.N., Knight J.C., Chizhikov V.E., Parsons J.M., Seliavanov N.A., Shchelkunov S.N., Eposito J.J.;

RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.

RN (4)

RP SEQUENCE FROM N.A.

RC STRAIN=Garcia-1966;

RX MEDLINE=20107289; PubMed=10639322;

RA Shchelkunov S.N., Totemuh A.V., Loparev V.N., Saifonov P.F., Gutarov V.V., Chizhikov V.E., Knight J.C., Parsons J.M., Masung R.F., Eposito J.J.;

RT "Alaetrim smallpox variola minor virus genome DNA sequences.";

RL Virology 266:361-386(2000).

RN (5)

RP SEQUENCE FROM N.A.

RC STRAIN=Butler-1952, Chimp 9-4, Garcia-1966, and Somalia-1977;

RA Loparev V.N., Parsons J.M., Eposito J.J.;

RT "DNA sequence analysis as a criterion for allocation of the orthopoxviruses to a particular species.";

RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.

RT FUNCTION: Receptor for TNF-alpha and TNF-beta. May contribute to the modification of TNF-mediated antiviral processes (By similarity).

CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).

CC -1- SIMILARITY: CONTAINS 2 TNFR-CYS REPEATS.

CC -----

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CC -----

CC EMBL; X69198; CAA49137.1; -.

DR EMBL; X67117; CAA47540.1; -

DR EMBL; L22579; AAA60933.1; -

DR EMBL; U18339; AAA69407.1; -

DR EMBL; U18341; AAA69467.1; -

DR EMBL; Y16780; CAB54728.1; -

DR EMBL; U88146; AAB94371.1; -

DR EMBL; U88148; AAB94373.1; -

DR EMBL; U88149; AAB94374.1; -

DR EMBL; U88152; AAB94377.1; -

DR PIR; D36858; D36858.

DR PIR; S35987; S35987.

DR PIR; S46888; S46888.

DR HSSP; O14763; 1D0G.

DR InterPro; IPR001368; TNFR_c6.

DR Pfam; PF00020; TNFR_c6; 2_

DR ProDom; PD000771; TNFR_c6; 1.

DR SMART; SM00208; TNFR_2.

DR PROSITE; PS00652; TNFR_NGFR_1; 2.

DR PROSITE; PS00650; TNFR_NGFR_2; 2.

KM Receptor; Glycoprotein; Repeat; Signal.

FT SIGNAL 1 22

FT CHAIN 23 349

FT REPEAT 31 66

FT REPEAT 67 108

FT DISULFID 32 43

FT DISULFID 44 57

FT DISULFID 47 65

FT DISULFID 68 83

FT DISULFID 86 100

FT DISULFID 90 108

FT CARBOHYD 101 101

FT CARBOHYD 173 173

FT CARBOHYD 189 189

FT CARBOHYD 215 215

FT CARBOHYD 248 248

FT VARIANT 17 17

FT VARIANT 160 160

FT VARIANT 165 165

FT VARIANT 182 182

FT VARIANT 274 274

FT VARIANT 335 335

FT VARIANT 339 339

FT SEQUENCE 349 AA; 38189 MW; D45D40B5C6E780EF CRC64;

SO

Query Match 17.4%; Score 260; DB 1; Length 349;

Best Local Similarity 32.2%; Pred. No. 1,3e-13;

Matches 59; Conservative 26; Mismatches 90; Indels 8; Gaps 3;

QY 5 PTYPWDAAE-TGERLVAOCAPGTFVQPCRDSPPTCGPCPPRHAYTOFWNNYLERGRYCN 63

Db PNRKCKDTEYKRNRLCLSPPTVASRLCDSKTNOCPTCGSGTTSRNHLPALCLSCN 87

QY 64 VLGERBEERACHATHNRACRCRTGPF-----AHAGFLEHASCPPGAGVYAPGPSQ 117

Db GRGNSNQVETRSCNTHNRNICESPAYCYLKGSSCKACVSGTKGIGYV-SGHTSVG 146

QY 118 NTCOCPCPTGTFASSSSBQCOPHRNCTALGLALNVPSSSHDTLCTSGTGFPLSTRP 177

Db DVICSPCGRTYSHVTSADKCEPVNNTFNVIDETILYPVNDICTRTTTTGSLSEL 206

QY 178 GAE 180

Db 207 TSE 209

RESULT 12

CRMB_CAMPS STANDARD; PRT; 349 AA.

AC Q8UYA7;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Soluble TNF receptor II precursor (cytokine response modifying protein
 DE B).
 GN [CRMB1 OR CMP2L OR CMLV002] AND (CRMB2 OR CMP205R OR CMLV210).
 OS Camelpox virus (strain CWS), and
 OS Camelpox virus (strain M-96).
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Orthopoxvirus.
 OX NCBI_TaxID=203172, 203173;
 RN [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN=CWS;
 RX PubMed=11907336;
 RA Gubser C., Smith G.L.;
 RT "The sequence of camelpox virus shows it is most closely related to
 RT variola virus, the cause of smallpox.";
 RL J. Gen. Virol. 83:855-872(2002).
 RN [2]
 RN SEQUENCE FROM N.A.
 RP STRAIN=M-96;
 RA Afonso C.L., Tulman E.R., Lu Z., Zaitsev V.L.,
 RA Kerembekova U.Z., Sandyaev N.T., Kutish G.F., Rock D.L.;
 RT "The genome of camelpox virus.";
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Receptor for TNF-alpha and TNF-beta. May contribute to
 CC the modification of TNF-mediated antiviral processes (By
 CC similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
 CC -!- SIMILARITY: CONTAINS 2 TNFR-CYS REPEATS.
 CC
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 CC
 CC -----
 CC EMBL; AY009089; A837456.1; -
 CC EMBL; AY009089; A837718.1; -
 CC EMBL; AF438165; AAL73920.1; -
 CC EMBL; AF438165; AAL73917.1; -
 CC InterPro: IPR001368; TNFR_C6.
 CC Pfam; PF00020; TNFR_C6; 2.
 CC SMART; SM00208; TNFR; 3.
 CC PROSITE; PS00652; TNFR_NGFR_1; 2.
 CC PROSITE; PS00652; TNFR_NGFR_2; 2.
 KW Receptor; Glycoprotein; Repeat; signal.
 FT SIGNAL 1 19 POTENTIAL.
 FT CHAIN 20 349 SOLUBLE TNF RECEPTOR II.
 FT REPEAT 31 65 TNFR-CYS 1.
 FT REPEAT 67 108 TNFR-CYS 2.
 FT DISULFID 32 43 BY SIMILARITY.
 FT DISULFID 44 57 BY SIMILARITY.
 FT DISULFID 47 65 BY SIMILARITY.
 FT DISULFID 68 83 BY SIMILARITY.
 FT DISULFID 86 100 BY SIMILARITY.
 FT DISULFID 90 108 BY SIMILARITY.
 FT CARBOHYD 101 101 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 189 189 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 248 248 N-LINKED (GLCNAC...) (POTENTIAL).
 CC SEQUENCE 349 AA; 38064 MW; EA412AF991E087F3 CRC64;
 Query Match 17.3%; Score 257.5; DB 1; Length 349;
 Best Local Similarity 32.0%; Pred. No. 2e-13;
 Matches 54; Conservative 28; Mismatches 80; Indels 7; Gaps 2;
 QY 18 LVCAQCPGPFVORCRDRSPTTCGPPRRHYTFQFMYLRCRYCNVLCGEREEARACH 77
 DB 42 LCLLSCPPGYASLCLDSKNTKTCPTGSGTFTSRNNHLPACLSCNCRCDNQVETRSCN 101

QY 78 ATHNRACRRTGTFP-----AHAGFCLEHASCPPGAGVIAPGTPSQNTQCPGCTFSA 131
 DB 102 TTHNRICEPSGYCILKSGCKACVSKTGIGYGV-SGHTSAGDVICSPCGLGTYSR 160
 QY 132 SSSSSQCCOPHRNCTALGLALNVPGSSSHDTLCTCTGFPPLSTRVPGAEE 180
 DB 161 TVSSADKCEPVSNTFNVDINLPVNDTCTRTTTTGISISITSE 209
 RESULT 13
 ID_CRM COMPX STANDARD; PRT; 351 AA.
 AC Q73559;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Soluble TNF receptor II precursor (cytokine response modifying protein
 DE B).
 GN [CRMB1 OR D2L] AND (CRMB2 OR H4R).
 OS Cowpox virus (CPV).
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Orthopoxvirus.
 OX NCBI_TaxID=10243;
 RN [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN=GRI-90 / Grishak;
 RX MEDLINE=98229462; PubMed=9568042;
 RA Shchelkunov S.N., Safonov V.V., Totmenin A.V., Petrov N.A.,
 RA Ryazankina O.I., Gutorov V.V., Kotwal G.J.;
 RT "The genomic sequence analysis of the left and right species-specific
 RT terminal region of a cowpox virus strain reveals unique sequences and
 RT a cluster of intact ORFs for immunomodulatory and host range
 RT proteins.";
 RL Virology 243:432-460(1998).
 RN [2]
 RN FUNCTION.
 RP STRAIN=Brighton red;
 RX PubMed=8091665;
 RA Hu F.Q., Smith C.A., Pickup D.J.;
 RT "Cowpox virus contains two copies of an early gene encoding a soluble
 RT secreted form of the type II TNF receptor.";
 RL Virology 204:343-356(1994).
 CC -!- FUNCTION: Receptor for TNF-alpha and TNF-beta. May contribute to
 CC the modification of TNF-mediated antiviral processes.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: CONTAINS 2 TNFR-CYS REPEATS.
 CC
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 CC
 CC -----
 CC EMBL; Y11842; CAA72578.1; -
 CC EMBL; Y15035; CAA75306.1; -
 CC HSP; O14763; IDOG.
 DR InterPro: IPR001368; TNFR_C6.
 DR Pfam; PF00020; TNFR_C6; 2.
 DR SMART; SM00208; TNFR; 2.
 DR PROSITE; PS00652; TNFR_NGFR_1; 2.
 DR PROSITE; PS00652; TNFR_NGFR_2; 2.
 KW Receptor; Glycoprotein; Repeat; signal.
 FT SIGNAL 1 19 POTENTIAL.
 FT CHAIN 20 351 SOLUBLE TNF RECEPTOR II.
 FT REPEAT 31 67 TNFR-CYS 1.
 FT REPEAT 69 110 TNFR-CYS 2.
 FT DISULFID 32 43 BY SIMILARITY.
 FT DISULFID 44 57 BY SIMILARITY.
 FT DISULFID 47 67 BY SIMILARITY.
 FT DISULFID 70 85 BY SIMILARITY.

QY 20 CAQCPGTFVQRCRDRSPPTTCGPPRRHYTOFWNYLER---CRYCNVLGGEREEARAC 76
 Db 54 CPKSPGYRKEACGELTGTVCEPCPGTVAHLNGLSKLQCMQCDPAMGLR--ASRNC 111
 QY 77 HATHNRACRRTGFFA-----HAGFLEHASCPPGAGVAPGPPSONTOCQCPPTGTF 130
 Db 112 SRTNNAVCGSPGHFCIVQDGDHCAACRAVATSPGQVKGGTESQDTLCQNCPPPTFS 171
 QY 131 ASSSSSQCPHNRCTALGALANVPGSSS 160
 Db 172 -PNTLEECQHQTKCSMLVTKAGATSSS 200

RESULT 15
 TR11_HUMAN
 ID TR11_HUMAN STANDARD; PRT; 616 AA.
 AC QY606;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 11A precursor
 DE (Receptor activator of NF-KB) (Osteoclast differentiation factor
 DE receptor) (ODFR)
 GN TNFRSF11A OR RANK.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Dendritic cell;
 RA MEDLINE=98032977; PubMed=9367155;
 RA Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C.,
 RA Tometsko M.E., Roux E.R., Tepe M.C., DuBoise R.F., Cosman D.,
 RA Galibert L.;
 RA "A homologue of the TNF receptor and its ligand enhance T-cell growth
 RT and dendritic-cell function.";
 RL Nature 390:175-179 (1997).
 RN [2]
 RP FUNCTION.
 RX MEDLINE=99097247; PubMed=9878548;
 RA Nakagawa N., Kinoshita M., Yanaguchi K., Shima N., Yasuda H., Yano K.,
 RA Morinaga T., Higashio K.;
 RA "RANK is the essential signaling receptor for osteoclast
 RT differentiation factor in osteoclastogenesis.";
 RL Biochem. Biophys. Res. Commun. 253:395-400 (1998).
 RN [3]
 RP VARIANT FEO 16-L-L-21 DUPL, VARIANT PDB2 13-A-L-21 DUPL, AND VARIANT
 RP V-192.
 RX MEDLINE=20082806; PubMed=10615125;
 RA Hughes A.E., Ralston S.H., Marken J., Bell C., MacPherson H.,
 RA Wallace R.G.H., van Hul W., Whyte M.P., Nakatsuka K., Hovy L.,
 RA Anderson D.M.;
 RT "Mutations in TNFRSF11A, affecting the signal peptide of RANK, cause
 RT familial expansile osteolysis.";
 RL Nat. Genet. 24:45-48 (2000).
 CC -!- FUNCTION: Receptor for TNFSF11/RANKL/TRANCE/OPGL; essential for
 CC RANKL-mediated osteoclastogenesis. Involved in the regulation of
 CC interactions between T-cells and dendritic cells.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
 CC -!- TISSUE SPECIFICITY: UBIQUITOUS EXPRESSION WITH HIGH LEVELS IN
 CC SKELETAL MUSCLE, THYMUS, LIVER, COLON, SMALL INTESTINE AND ADRENAL
 CC GLAND.
 CC -!- DISEASE: DEFECTS IN TNFRSF11A ARE THE CAUSE OF FAMILIAL EXPANSILE
 CC OSTEOLYSIS (FEO), A RARE AUTOSOMAL DOMINANT BONE DISORDER
 CC CHARACTERIZED BY FOCAL AREAS OF INCREASED BONE REMODELLING. THE
 CC OSTEOCLYTIC LESIONS DEVELOP USUALLY IN THE LONG BONES DURING EARLY
 CC ADULTHOOD. FEO IS OFTEN ASSOCIATED WITH EARLY ONSET DEAFNESS AND
 CC LOSS OF DENTITION.
 CC -!- DISEASE: DEFECTS IN TNFRSF11A ARE A CAUSE OF FAMILIAL PAGET
 CC DISEASE OF BONE, ALSO KNOWN AS PAGET DISEASE OF BONE 2 (PDB2). IT
 CC IS A BONE REMODELLING DISORDER WITH CLINICAL SIMILARITIES TO FEO.
 CC UNLIKE FEO, HOWEVER, AFFECTED INDIVIDUALS HAVE INVOLVEMENT OF THE

CC AXIAL SKELETON WITH LESIONS IN THE SPINE, PELVIS AND SKULL.
 CC -!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
 CC -----
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 CC -----
 DR EMBL; AF018253; AAB86809.1; -;
 DR HSSP; P25942; ICDP; TNFRSF11A.
 DR Genew; HGNC:11908; TNFRSF11A.
 DR MIM; 603499; -;
 DR MIM; 174810; -;
 DR MIM; 602080; -;
 DR InterPro: IPR001368; TNFR_c6.
 DR Pfam; PF00020; TNFR_c6; 4.
 DR ProDom; PD000771; TNFR_c6; 1.
 DR SMART; SM00208; TNFR; 4.
 DR PROSITE; PS00652; TNFR_NGFR_1; 1.
 DR PROSITE; PS00050; TNFR_NGFR_2; 1.
 KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal; Polymorphism;
 KW Disease mutation.
 FT SIGNAL 1 29 POTENTIAL.
 FT CHAIN 30 616 TUMOR NECROSIS FACTOR RECEPTOR
 FT SUPERFAMILY MEMBER 11A.
 FT EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 30 212 POTENTIAL.
 FT TRANSMEM 213 233 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 234 616 TNFR-CYS 1.
 FT REPEAT 34 68 TNFR-CYS 2.
 FT REPEAT 71 112 TNFR-CYS 3.
 FT REPEAT 114 151 TNFR-CYS 4.
 FT REPEAT 154 194 BY SIMILARITY.
 FT DISULFID 34 46 BY SIMILARITY.
 FT DISULFID 47 60 BY SIMILARITY.
 FT DISULFID 50 68 BY SIMILARITY.
 FT DISULFID 71 86 BY SIMILARITY.
 FT DISULFID 92 112 BY SIMILARITY.
 FT DISULFID 114 127 BY SIMILARITY.
 FT DISULFID 133 151 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 105 105 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 174 174 L-LINKED (GLCNAC...) (POTENTIAL).
 FT VARIANT 21 21 L -> LALLCALL (IN PDB2).
 FT VARIANT 21 21 /FTid=VAR_011516.
 FT VARIANT 21 21 L -> LLLCALL (IN FEO).
 FT VARIANT 192 192 /FTid=VAR_011517.
 FT VARIANT 192 192 A -> V.
 FT SEQUENCE 616 AA; 66033 MW; E3DE9A7A08196F81 CRC64;
 SQ Query Match 15.8%; Score 235.5; DB 1; Length 616;
 Best Local Similarity 31.3%; Pred. No. 1.9e-11;
 Matches 52; Conservative 26; Mismatches 77; Indels 11; Gaps 4;
 QY 20 CAQCPGTFVQRCRDRSPPTTCGPPRRHYTOFWNYLERC---RYCNVLGGEREEARAC 76
 Db 47 CNKCEPKYWSKCTTTSDSVCLPCGPDVLDSDWNEEDKLLHKVCDT--GKALVAVVAG 104
 QY 77 HATHNRACRRTGFF--AHAGFLEHASCPPGAGVATGTPSONTOCQCPPTGTFSSSS 134
 Db 105 NSTTPRCACATAGYHWSQDCCECCRRNTECAPGLGAQHPQLNKNKDTVCKPLAGYFSAFS 164
 QY 135 SSEQCQPHRNTALGALANVPGSSSHDTLCTCTGFPPLSTRVPGAE 180
 Db 165 STDKCRWTNCTFLGKKEVHGTEKSDAVCSS-----SLPARKPNE 206

Search completed: January 6, 2003, 11:18:40
 Job time : 23 secs

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OM protein - nucleic search, using frame_plus.p2n model

Run on: January 6, 2003, 11:26:15 ; Search time 51 Seconds

(without alignments)
1629.596 Million cell updates/sec

Title: US-09-936-024-1

Perfect score: 1491

Sequence: 1 VAEPTPYMRDAETGERLVC.....RVAMPGLERSVEREFLPVH 271

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODER-frame.p2n.model -DEV=x1h
-Q=/cgn2_1/USPTO.spool/US09936024/runat_06012003_111607_12151/app_query.fasta_1.455
-DB=Issued Patents NA -QFMT=fastap -SUFIX=p2n.rni -MINMATCH=0.1 -LOOPL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pct -NCRMe=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USFR=US09936024.@cgn_1_1.25@runat_06012003_111607_12151 -NCPU=6 -ICPU=3
-NO XLIFY -NO WMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THEADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued Patents NA.*
1: /cgn2_6/prodata/2/ina/5A_COMB.seq.*
2: /cgn2_6/prodata/2/ina/5B_COMB.seq.*
3: /cgn2_6/prodata/2/ina/6A_COMB.seq.*
4: /cgn2_6/prodata/2/ina/6B_COMB.seq.*
5: /cgn2_6/prodata/2/ina/PCUTS_COMB.seq.*
6: /cgn2_6/prodata/2/ina/backfile1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1491	100.0	1164	2	US-08-794-796-1
2	1491	100.0	1347	4	US-09-286-529-18
3	1339	89.8	1859	4	US-09-286-529-19
4	841	56.4	459	4	US-09-286-529-7
5	440.5	29.5	1355	3	US-08-974-022-5
6	440.5	29.5	1355	4	US-08-795-445A-5
7	440.5	29.5	1355	4	US-08-795-447A-5
8	440.5	29.5	1355	4	US-08-974-186-5
9	440.5	29.5	1355	4	US-08-795-446B-5
10	440.5	29.5	1355	4	US-08-706-945D-127
11	433	29.0	525	3	US-08-997-918-47
12	425.5	28.5	2432	3	US-08-974-022-1

13	425.5	28.5	2432	4	US-08-795-445A-1	Sequence 1, Appl1
14	425.5	28.5	2432	4	US-08-795-447A-1	Sequence 1, Appl1
15	425.5	28.5	2432	4	US-08-974-186-1	Sequence 1, Appl1
16	425.5	28.5	2432	4	US-08-795-446B-1	Sequence 1, Appl1
17	425.5	28.5	2432	4	US-08-706-945D-123	Sequence 123, App
18	424.5	28.5	1324	3	US-08-974-022-3	Sequence 3, Appl1
19	424.5	28.5	1324	4	US-08-795-445A-3	Sequence 3, Appl1
20	424.5	28.5	1324	4	US-08-795-447A-3	Sequence 3, Appl1
21	424.5	28.5	1324	4	US-08-974-186-3	Sequence 3, Appl1
22	424.5	28.5	1324	4	US-08-795-446B-3	Sequence 3, Appl1
23	424.5	28.5	1324	4	US-08-706-945D-125	Sequence 125, App
24	344.5	23.1	1557	1	US-08-585-229-3	Sequence 3, Appl1
25	342	22.9	1641	1	US-08-650-000-1	Sequence 1, Appl1
26	342	22.9	1641	6	5395760-1	Patent No. 5395760
27	342	22.9	2224	4	US-08-477-347-2	Sequence 2, Appl1
28	342	22.9	2224	4	US-08-476-862-1	Sequence 1, Appl1
29	342	22.9	3683	4	US-09-844-634-3	Sequence 1, Appl1
30	340	22.8	705	4	US-09-326-394-3	Sequence 3, Appl1
31	338	22.7	705	4	US-09-580-235-1	Sequence 1, Appl1
32	338	22.7	705	4	US-09-580-235-1	Sequence 1, Appl1
33	338	22.7	705	4	US-09-580-181-1	Sequence 7, Appl1
34	338	22.7	705	4	US-09-580-181-1	Sequence 7, Appl1
35	338	22.7	705	4	US-09-580-181-7	Sequence 7, Appl1
36	338	22.7	705	4	US-09-102-530-1	Sequence 1, Appl1
37	338	22.7	705	4	US-09-102-530-7	Sequence 7, Appl1
38	337	22.6	705	4	US-09-580-235-3	Sequence 3, Appl1
39	337	22.6	705	4	US-09-580-235-5	Sequence 5, Appl1
40	337	22.6	705	4	US-09-580-181-3	Sequence 3, Appl1
41	337	22.6	705	4	US-09-580-181-5	Sequence 5, Appl1
42	337	22.6	705	4	US-09-102-530-3	Sequence 3, Appl1
43	337	22.6	705	4	US-09-102-530-5	Sequence 5, Appl1
44	332.5	22.3	3796	2	US-08-762-308-11	Sequence 11, Appl1
45	332.5	22.3	3796	4	US-09-844-634-10	Sequence 10, Appl1

ALIGNMENTS

RESULT 1
US-08-794-796-1
Sequence 1, Application US/08794796
Patent No. 5885800
GENERAL INFORMATION:
APPLICANT: Emery, John
APPLICANT: Tan, KB
APPLICANT: Truneh, Alem
TITLE OF INVENTION: Tumor Necrosis Related Receptor,
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/794, 796
FILING DATE: 04-FEB-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Han, William T
REGISTRATION NUMBER: 34,344
REFERENCE/DOCKET NUMBER: GH50000
TELECOMMUNICATION INFORMATION:

TELEPHONE: 610-270-5219
TELEFAX: 610-270-4026
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1164 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-794-796-1

Alignment Scores:
Pred. No.: 1,25e-109 Length: 1164
Score: 1491.00 Matches: 271
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-936-024-1 (1-271) x US-08-794-796-1 (1-1164)

QY 1 ValAlaGluThrProThrTyrProTrpArgAspAlaGluThrGlyGluArgLeuValCys 20
DB 198 GTGGCAGAAACACCCACCTACCTCGCGGACGCAGACAGCGGGCGGTGGTGTGC 257
QY 21 AlaGlnCysProGlyThrPheValGlnArgProCysArgArgAspSerProThrThr 40
DB 258 GCCCAGTGGCCCCCAGGCACCTTTGTGACGGCGCGTGGCGCGAGACAGCCCCACGAGC 317
QY 41 CysGlyProCysProProArgHisTyrThrGlnPheTrpAsnTyrLeuGluArgCysArg 60
DB 318 TGTGGCCCCGTGCACCGCGCCACTACACGAGTTCTGGAACTACCTGGAGCGCTCCGC 377
QY 61 TyrCysAsnValLeuCysGlyGluArgGluGluAlaArgAlaCysHisAlaThrHis 80
DB 378 TACTGCAACGTCTCTCGGGGAGCGTGAGGAGGAGCAGCGGCTTGCACGCCACCCAC 437
QY 81 AsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHis 100
DB 438 AACCGTGCTCGCGCTCGCCACCGGCTTCTCGCGACGCTTGTCTGCTTGGAGCAC 497
QY 101 AlaSerCysProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGln 120
DB 498 GCATGTGTCCACTGTGTGGCGCGTGATTGCCCGGGCACCCCCAGCAGACACGAG 557
QY 121 CysGlnProCysProGlyThrPheSerAlaSerSerSerSerGluGlnCysGln 140
DB 558 TGCACGCCGTGCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTCCAG 617
QY 141 ProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerHis 160
DB 618 CCCACCGCAACTGCACGGCCCTGGGCGCTGGGCGCTCAATGTGCAGGCTCTTCTCCCAT 677
QY 161 AspThrLeuCysThrSerCysThrGlyPheProLeuSerThrArgValProGlyAlaGlu 180
DB 678 GACACCTGTGCACCAAGCTGCATGGCTTCCCTCAGCACCAGGGTACAGAGGCTGAG 737
QY 181 GluCysGluArgAlaValIleAspPheValAlaPheGlnAspIleSerIleCysArgLeu 200
DB 738 GAGTGTGAGCGTGCCTCATCGACTTGTGGCTTCCAGGACATCTCCATCAAGAGGCTG 797
QY 201 GlnArgLeuLeuGlnAlaLeuGluAlaProGluGlyTyrGlyProThrProArgAlaGly 220
DB 798 CAGCGGCTGTGACGGCCCTCGAGGCCCGCGAGGGCTGGGGTCCGACACCAAGGGGGGC 857
QY 221 ArgAlaAlaLeuGlnLeuLysLeuArgArgArgLeuThrCluLeuLeuGlyAlaGlnAsp 240
DB 858 CGCGGGCTGTGACGTGAAGCTGCGTGGCGGGCTCACGAGCTCTCTGGGGCGCAGGAC 917
QY 241 GlyAlaLeuLeuValArgLeuLeuGlnAlaLeuArgValAlaArgMetProGlyLeuGlu 260
DB 918 GGGGCGCTGCTGTGGTGTGCTGACAGGCGCTGCGGCTGGCCAGGATGCCCGGGCTGGAG 977

QY 261 ArgSerValArgGluArgPheLeuProValHis 271
DB 978 CGGAGCGTCCGTGAGCGCTTCTCCTGTGCAC 1010

RESULT 2

US-09-286-529-18
Sequence 18, Application US/09286529
Patent No. 6297367
GENERAL INFORMATION:
APPLICANT: Catherine Tribouley
TITLE OF INVENTION: NEW MEMBERS OF TNF AND TNFR FAMILIES
FILE REFERENCE: 1408.003/200130.439C1
CURRENT APPLICATION NUMBER: US/09/286,529
CURRENT FILING DATE: 1999-04-05
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 18
LENGTH: 1347
TYPE: DNA
ORGANISM: Homo sapien
US-09-286-529-18

Alignment Scores:
Pred. No.: 1,53e-109 Length: 1347
Score: 1491.00 Matches: 271
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-936-024-1 (1-271) x US-09-286-529-18 (1-1347)

QY 1 ValAlaGluThrProThrTyrProTrpArgAspAlaGluThrGlyGluArgLeuValCys 20
DB 405 GTGGCAGAAACACCCACCTACCTCGCGGACGCAGACAGCGGGCGGTGGTGTGC 464
QY 21 AlaGlnCysProGlyThrPheValGlnArgProCysArgArgAspSerProThrThr 40
DB 465 GCCCAGTGGCCCCCAGGCACCTTTGTGACGGCGCGTGGCGCGAGACAGCCCCACGAGC 524
QY 41 CysGlyProCysProProArgHisTyrThrGlnPheTrpAsnTyrLeuGluArgCysArg 60
DB 525 TGTGGCGCGTGTCCACCGCGCCACTACACGCACTTCTGGAACCTACTGTGAGCGCTGCCGC 584
QY 61 TyrCysAsnValLeuCysGlyGluArgGluGluGluAlaArgAlaCysHisAlaThrHis 80
DB 585 TACTCAACGTCTCTCGGGGAGCGTGAGGAGGAGGACCGGCTTGCACGCCACCCAC 644
QY 81 AsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHis 100
DB 645 AACCGTGCTGCGCTGCGCAGCCGCTTCTTCGCGCACGCTTCTGCTTGGAGCAC 704
QY 101 AlaSerCysProGlyValIleAlaProGlyThrProSerGlnAsnThrGln 120
DB 705 GCATGTGTCCACTGTGTGGCGCGTGATTGCCCGGGCACCCCCAGCCAGAACACGAGCAG 764
QY 121 CysGlnProCysProProGlyThrPheSerAlaSerSerSerSerGluGlnCysGln 140
DB 765 TGCCAGCGCTGCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCACAG 824
QY 141 ProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerHis 160
DB 825 CCCCCCGCAACTGCACGGCCCTGGGCGCTCAATGTGCCAGGCTCTTCTCTCCCAT 884
QY 161 AspThrLeuCysThrSerCysThrGlyPheProLeuSerThrArgValProGlyAlaGlu 180
DB 885 GACACCTGTGCACCGCTGCATGGCTTCCCGCTCAGCACCGGGTACCAGGAGCTGAG 944
QY 181 GluCysGluArgAlaValIleAspPheValAlaPheGlnAspIleSerIleLysArgLeu 200
DB 945 GAGTGTGAGCGTGGCGCTCATCGACTTTGTGGCTTTCAGGACATCTCCATCAAGAGGCTG 1004

QY 201 GlnArgLeuLeuGlnAlaLeuGlnAlaProGluGlyTyrGlyProThrProArgAlaGly 220
Db 1005 CAGGGGCTGCTGAGGCGCTCGAGGCGCCGAGGGGCTGGGGTCCGACACCAAGGGCGGGC 1064
QY 221 ArgAlaAlaLeuGlnLeuLeuLeuArgArgArgLeuThrGluLeuGlyAlaGlnAsp 240
Db 1065 CGCGCGGCTTGACAGCTGAGTGGGCGGCTCACGAGGCTTCGGGGGCGGACGAGC 1124
QY 241 GlyAlaLeuLeuValArgLeuLeuGlnAlaLeuArgValAlaArgMetProGlyLeuGlu 260
Db 1125 GGGGCGCTGCTGCTGCGGCTGCTGCGAGGCGCTGCGGCTGCGGATGCGGGGCTGAG 1184
QY 261 ArgSerValArgGluArgPheLeuProValHis 271
Db 1185 CGAGCGCTCGTGAGCGCTCTCCCTGTGCAC 1217
RESULT 3
US-09-286-529-19
; Sequence 19, Application US/09286529
; Patent No. 6297367
; GENERAL INFORMATION:
; APPLICANT: Catherine Tribouley
; TITLE OF INVENTION: NEW MEMBERS OF TNF AND TNFR FAMILIES
; FILE REFERENCE: 1408.003/200130.439C1
; CURRENT APPLICATION NUMBER: US/09/286,529
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PaateSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 1859
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-286-529-19
Alignment Scores:
Pred. No.: 2,696-97 Length: 1859
Score: 1339.00 Matches: 271
Percent Similarity: 51.72% Conservative: 0
Best Local Similarity: 51.72% Mismatches: 0
Query Match: 89.81% Indels: 253
DB: 4 Gaps: 1
US-09-936-024-1 (1-271) x US-09-286-529-19 (1-1859)
QY 1 ValAlaGluThrProThrTyrProThrPheArgPheAlaGluThrGlyGluArgLeuValCys 20
Db 165 GTGGCGAGAAACACCCACTACCTCGCGGAGCGAGACAGAGAGGAGCGGCTGGTGGC 224
QY 21 AlaGlnCysProProGlyTyrPheValGlnArgProCysArgArgAspSerProThrThr 40
Db 225 GCCCAGTCCCGCCAGGACCTTTGTGAGGCGGCGGCTGCCGAGACAGCCCAAGCAG 284
QY 41 CysGlyProCysProProArgHisTyrThrGlnPheTyrPheTyrLeuGluArgCysArg 60
Db 285 TGTGGCCCGTGTCCACCGCGCACCTACGAGGAGTTCTGAACTACTGAGACGCTGCCG 344
QY 61 TyrCysAsnValLeuCysGlyGluArgGluGluGluAlaArgAlaCysHisAlaThrHis 80
Db 345 TACGCAACGCTCTGTGGGAGGAGGTAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 404
QY 81 AsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHis 100
Db 405 AACCGTGGCTCCGCTGCGGACCGGCTTTCTTCGCGACGCTGTTTCTTGAGAGAC 464
QY 101 AlasercysProProGlyValGlyValIleAlaProGlyTyrProSerGlnAsnThrGln 120
Db 465 GCATCGTGTCCACCTGTGCGGCGGTGATTGCCCGGAGCAACCCAGCAAGAACAGCAG 524
QY 121 CysGlnProCysProProGlyTyrPheSerAlaSerSerSerSerSerSerSerSerSer 140
Db 525 TGCCAGCCGTCGCCCGGAGGACCTTCTCAGCCAGCACTCCAGCTCAGACAGGAGCCAG 584
QY 141 ProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerSerHis 160

Db 585 CCCCACCGCAACTGCAAGGCGCTGGGCGCTGGCCCTCATGTGCGAGGCTCTTCTCCAT 644
QY 161 AspThrLeuCysThrSerCysThrGlyPheProLeuSerHisArgValPro----- 177
Db 645 GACACCTGTGACACCACTGACTGCTTCCCTTCAGCACAGGATACAGGTAGACCA 704
QY 177 ----- 177
Db 705 GAGGCTGAGGGGGGACACACACTGACAGGCCAGGCCACTTGTGCTCCTCACTCTGCCCT 764
QY 177 ----- 177
Db 765 GACAGTCATCTAGCTTGAGGATGACAGCTGGCTTGGAAGGGGACAGTGATTTG 824
QY 177 ----- 177
Db 825 AGGGTCAGGGGTCCTCCACTAGATCCCAAGTCTGCTTCAGAGGGGTGGCTGAG 884
QY 177 ----- 177
Db 885 AATTGGATCTGAGCCAGGACAGCTCCCTGGAGAGCTCTGGAAAGTGGGACGAA 944
QY 177 ----- 177
Db 945 TCTCTAATGCCCCGAGGGAGAGGTGGCTGCTCTCTGACAGGGGAAACGAGGCTG 1004
QY 177 ----- 177
Db 1005 ATGTAAATCTCTTAAGTCTGAGAGAGGTGGCTGCTCTCTGACATGGGAAAC 1064
QY 177 ----- 177
Db 1065 GAGGCCCAATGTTAACCACTGTTGAGAAATCACAGGGGGAATGACCCCTTAATCA 1124
QY 177 ----- 177
Db 1125 GTGAGTCCGGTTCATGTGAGGTCCTCAACTCGCCCTTCGATGGCCAGAGCCCA 1184
QY 177 ----- 177
Db 1185 GCCCTGCTGGGCGCCCTTCTCTTTCAGCAAGGTCCGAGTCCGCTCTGCCCC 1244
QY 177 ----- 177
Db 1245 TAGGCTTTGCTCAGCTCTCTGACGAGGCTCTGCTCTCTCCATGCCATCCTT 1304
QY 177 ----- 177
Db 1305 GCACTGCCCTCTCAGACGCGCTCAGTCAAGGATTTCTCTCTCTGCAACCCCCC 1364
QY 177 ----- 177
Db 1365 AGTGGGCGCCAGAAAGAGGATCTTGACAGCCCGCCAGTGTGTGTGTAATAAT 1424
QY 178 -----GlyAlaGluGluCysGluArgAlaValIleAs 168
Db 1425 CGGACCGCTGCTCCCAACCCCACTGCAAGGAGCTGAGAGGTGAGGCTGCTCATCGA 1484
QY 188 PheValAlaPheGlnAspIleSerIleLeuArgLeuGlnAlaLeuGlnAlaLeuGln 208
Db 1485 CTTTGTGGCTTTCCAGACATCTTCATCAAGAGGCTGACAGGCTGTCAGGCGCTCGA 1544
QY 208 uAlaProGluGlyTyrGlyProThrProArgAlaGlyArgAlaAlaLeuGlnLeuLys 228
Db 1545 GGGCCCGAGGGGCTGGGGTCCGACACCAAGGGGCGGCGGCTTTCAGCTGAAGCT 1604
QY 228 uArgArgArgLeuThrGluLeuLeuGlyAlaGlnAspGlyAlaLeuLeuValArgLeu 248
Db 1605 GCGTGGCGGCTCAGAGCTCTCGGGGGGCGCAGAGAGGGGCGCTGTGTGTGGCTGCT 1664
QY 248 uGlnAlaLeuArgValAlaArgMetProGlyLeuGluArgSerValArgGluArgPhe 268

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Db 1665 GCAGCGCTGCGCTGCCAGGATGCCGGCTGGAGCGGAGCGCTCGTGAGCGCTTCCT 1724
Qy 268 uProValHis 271
| | | | |
Db 1725 CCCTGTGCAC 1734

RESULT 4
US-09-286-529-7
; Sequence 7, Application US/09286529
; Patent No. 6297367
; GENERAL INFORMATION:
; APPLICANT: Catherine Triboulev
; TITLE OF INVENTION: NEW MEMBERS OF TNF AND TNFR FAMILIES
; FILE REFERENCE: 1408.003/200130.439C1
; CURRENT APPLICATION NUMBER: US/09/286,529
; CURRENT FILING DATE: 1999-04-05
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 459
; TYPE: DNA
; ORGANISM: human
US-09-286-529-7

Alignment Scores:
Pred. No.: 1,21e-58 Length: 459
Score: 841.00 Matches: 153
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 56.41% Indels: 0
DB: 4 Gaps: 0

US-09-936-024-1 (1-271) x US-09-286-529-7 (1-459)
Qy 56 LeuGluArgCysArgTyrCysAsnValLeuCysGlyGluArgGluGluAlaArgAla 75
| | | | |
Db 1 CTGGAGCGCTGCCGCTACTGCAACGTCCTCTGCGGGAGCGTGAGGAGGCGACGGGCT 60

Qy 76 CysHisAlaThrHisAsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAlaGly 95
| | | | |
Db 61 TGCCAGCCACCCACACACCGCTGCGCGCTGCCGACCGGCTTCTTGGCGCACGCTGGT 120

Qy 96 PheCysLeuGluHisAlaSerCysProProGlyAlaGlyValIleAlaProGlyThrPro 115
| | | | |
Db 121 TTCTGCTTGAGCAGCGCATCGTGTCCACCTGGTCCCGCGCGTGATTGCCCGGCGACCCCC 180

Qy 116 SerGlnAsnThrGlnCysGlnProCysProGlyThrPheSerAlaSerSerSer 135
| | | | |
Db 181 AGCCAGNACAGGAGTGCCAGCGCTGCCCGCCCGCCAGGACCTTCTCAGCCAGCAGCTCAGC 240

Qy 136 SerGluGlnCysGlnProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValPro 155
| | | | |
Db 241 TCAGAGCAGTGCCAGCCACCCACCGCACTGCACGCGCTGGCGCTGCCCTCAATGTGCCA 300

Qy 156 GlySerSerSerHisAspThrLeuCysThrSerCysThrGlyPheProLeuSerThrArg 175
| | | | |
Db 301 GGCTCTTCTCCCATGACACCCCTGTGCACCGCTGCACCTGGCTTCCCTCCCTCAGCACCAGG 360

Qy 176 ValProGlyValAlaGluGluCysGluArgAlaValIleAspPheValAlaPheGlnAspIle 195
| | | | |
Db 361 GTACACGAGAGCTGAGGAGTGTTGAGCGTGCGCTCATCGACTTTGTGGCTTTCAGGACATC 420

Qy 196 SerIleLysArgLeuGlnArgLeuLeuGlnAlaLeuGlu 208
| | | | |
Db 421 TCATCAAGAGGCTGCAGCGGCTGCTGCAGGCCCTCGAG 459

RESULT 5
US-09-974-022-5
; Sequence 5, Application US/08974022
; Patent No. 6015938
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
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; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: OSTEOPROTEGERIN
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,022
; FILING DATE: 12-DEC-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/577,788
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-378
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1355 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 94...1296
US-08-974-022-5

Alignment Scores:
Pred. No.: 3,05e-26 Length: 1355
Score: 440.50 Matches: 77
Percent Similarity: 57.75% Conservative: 31
Best Local Similarity: 41.18% Mismatches: 74
Query Match: 29.54% Indels: 5
DB: 3 Gaps: 2

US-09-936-024-1 (1-271) x US-08-974-022-5 (1-1355)
Qy 5 ProThrTyrProTrpArgAspAlaGluThrGlyGluArgLeuValCysAlaGlnCysPro 24
| | | | |
Db 169 CCAAAGTACCTTCATTATGACGAAGAAACCTCTCATCAGCTGTGTGTGACAAATGTCT 228

Qy 25 ProGlyThrPheValGlnArgProCysArgArgAspSerProThrThrCysGlyProCys 44
| | | | |
Db 229 CTGTGTACTACTAAACACACACTGTACAGCAAGTGGAGAACCCGTGTGCCCTTGC 288

Qy 45 ProProArgHisTyrThrGlnPheTrpAsnTyrLeuGluArgCysArgTyrCysAsnVal 64
| | | | |
Db 289 CCTGACCCTACTACACAGACAGCTGGCACCAGTGCAGTGTCTATCTATCTGCAGCCCC 348

Qy 65 LeuCysGlyGluArgGluGluAlaArgAlaCysHisAlaThrHisAsnArgAlaCys 84
| | | | |
Db 349 GTGTGCAAGGAGCTGCAGTACGTCAAGCAGAGAGTGCATCGCACCCACCAACCGGTGTC 408

Qy 85 ArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHisAlaSerCysPro 104
| | | | |
Db 409 GAATGCAAGAGGCGCTTACCTTGAGATAGAGTCTCTGCTTGAACATAGGAGCTCCCT 468

Qy 105 ProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGlnCysGlnProCys 124
| | | | |
Db 469 CTGGATTGTGGAGTGTGCAAGCTGGNAACCCAGAGAGCGAAATACAGTTTGCACAAAGATGT 528

Qy 125 ProProGlyThrPheSerAlaSerSerSerSerGluGlnCysGlnProHisArgAsn 144
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Db 529 CCAAGATGGGTTCTTCTCAAAATGAGACGCTCACTTAAGCACCCCTGTAAACACACACAAAT 588
Qy 145 CyeThra1aleuGlYleuAlaleuAsnValProGlySerSerSerHisaePTnleuCyS 164
Db 589 TGCAGTGTCTTTGGTCTCCGCTAAGTACAGAAAGAAATGCACACGACGACACATA--- 645
Qy 165 ThSerCysThrglyPheProLeuSerThraYValProGlyAlaGluGlu-----Cys 182
Db 646 -----TGTCCGGAACAGTGAATCACTCAAAATGTGGAATAGATGTACCCCTGTGT 699
Qy 183 GluArgAlaValIleAspHe 189
Db 700 GAGAGGCAATCTTCAGGTTT 720
RESULT 6
US-08-795-445A-5
; Sequence 5, Application US/08795445A
; Patent No. 6284485
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: OSTEOPROTEGERIN
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/795,445A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/577,788
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-378
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1355 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 94..1296
; US-08-795-445A-5
Alignment Scores:
Pred. No.: 3.05e-26 Length: 1355
Score: 440.50 Matches: 77
Percent Similarity: 57.75% Conservative: 31
Best Local Similarity: 41.18% Mismatches: 74
Query Match: 29.54% Indels: 5
Gaps: 2
US-09-936-024-1 (1-271) x US-08-795-445A-5 (1-1355)
Qy 5 ProThrTyPProTfPaGAsPaAlaGluThrGlyGluArgLeuValCySAlaGluCySPro 24
Db 169 CCAAGTACCTTCACTATATGACGAAGAAACCTCTCATCAGCTGTGTGTGACAAATGTCTT 228

Qy 25 ProGlyThrPheValAlnArgProCySArgArgAspSerProThrThrCysGlyProCyS 44
Db 229 CCGTGTACTTACCTTAAACAACTGACGAAAGTGAAGACCGGTGCGCCCTTGC 288
Qy 45 ProProArgHisTyrThrglnPheTTPaerTyrLeuGluArgCySArgTyrCySAsnVal 64
Db 289 CCGACCACTACACACAGACAGCTGGCACACGACGATGTCTATCTCAGCCGCC 348
Qy 65 LeuCyGluGlyGluArgGluGluGluAlaArgAlaCySHisAlaThrHisAsnArgAlaCyS 84
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Db 409 GAATGCAGAGAGAGGCGGCTACTTGAAGATAGAGTTCTGCTGTAACATAGAGACTGCGCT 468
Qy 105 ProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrglnCysGlnProCyS 124
Db 469 CCGGATTTGGAGTGTGTCAGAGCTGGAACCCAGACGGAATACAGTTTGCAAAAGATGT 528
Qy 125 ProProGlyThrPheSerAlaSerSerSerSerSerGluGlnCysGlnProHisArgAsn 144
Db 529 CCAAGATGGGTTCTTCTCAAAATGAGACGCTCATCTTAAGCACCCCTGTGAAACACACAAAT 588
Qy 145 CyeThra1aleuGlYleuAlaleuAsnValProGlySerSerSerHisaePTnleuCyS 164
Db 589 TGCAGTGTCTTTGGTCTCCGCTAAGTACAGAAAGAAATGCACACGACGACACATA--- 645
Qy 165 ThSerCysThrglyPheProLeuSerThraYValProGlyAlaGluGlu-----Cys 182
Db 646 -----TGTCCGGAACAGTGAATCACTCAAAATGTGGAATAGATGTACCCCTGTGT 699
Qy 183 GluArgAlaValIleAspHe 189
Db 700 GAGAGGCAATCTTCAGGTTT 720
RESULT 7
US-08-795-447A-5
; Sequence 5, Application US/08795447A
; Patent No. 6284728
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: Osteoprotegerin
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Amgen Inc.
; STREET: One Amgen Center Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91362-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/795,447A
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-378D2
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1355 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

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; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 94...1296
US-08-795-447A-5

Alignment Scores:
Pred. No.: 3,05e-26 Length: 1355
Score: 440.50 Matches: 77
Percent Similarity: 57.75% Conservative: 31
Best Local Similarity: 41.18% Mismatches: 74
Query Match: 29.54% Indels: 5
DB: 4 Gaps: 2

US-09-936-024-1 (1-271) x US-08-795-447A-5 (1-1355)
QY 5 ProThrTyrProTrpArgAspAlaGluThrGlyGluArgLeuValCysAlaGlnCysPro 24
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QY 25 ProGlyThrPheValGlnArgProCysArgAspSerProThrThrCysGlyProCys 44
Db 229 CCTGGTACCTACCTAAACAACACTGTACAGCAAGTGGAGACCGGTGCGCCCTTGC 288
QY 45 ProProArgHisTyrThrGlnPheTrpAsnTyrLeuGluArgCysArgTyrCysAsnVal 64
Db 289 CCTGACCCTACTACACAGACAGCTGGCCACACCACTGACGAGTGTCTATACAGCCCC 348
QY 65 LeuCysGlyGluArgGluGluAlaArgAlaCysHisAlaThrHisAsnArgAlaCys 84
Db 349 GTGTGCAAGGAGTGCAGTACGTCACAGACAGTGCATCGACCCACACCCGCGTGTGC 408
QY 85 ArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHisAlaSerCysPro 104
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QY 125 ProProGlyThrPheSerAlaSerSerSerSerGluGlnCysGlnProHisArgAsn 144
Db 529 CCAGATGGGTCTCTCAATGAGACGTCATCTAAAGCACCTCTAAAGCACCCACACCAAT 588
QY 145 CysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerSerHisAspThrLeuCys 164
Db 589 TGCAGTGTCTTTTGTCTCTCTGCTAACTCAGAAAGGAAATGCAACACACGACACATA 645
QY 165 ThrSerCysThrGlyPheProLeuSerThrArgValProGlyAlaGluGlu-----Cys 182
Db 646 -----TGTTCCGGAACAGTGAATCAACTCAAAATGTGGAATAGATGTTACCTGTGT 699

RESULT 8
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; Sequence 5, Application US/08974186
; Patent No. 6284740
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: OSTEOPROTEGERIN
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESS: Amgen Inc.
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA

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; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,186
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/577,788
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-378
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1355 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 94...1296
US-08-974-186-5

Alignment Scores:
Pred. No.: 3,05e-26 Length: 1355
Score: 440.50 Matches: 77
Percent Similarity: 57.75% Conservative: 31
Best Local Similarity: 41.18% Mismatches: 74
Query Match: 29.54% Indels: 5
DB: 4 Gaps: 2

US-09-936-024-1 (1-271) x US-08-974-186-5 (1-1355)
QY 5 ProThrTyrProTrpArgAspAlaGluThrGlyGluArgLeuValCysAlaGlnCysPro 24
Db 169 CCAAAGTACCTTCATTATGACGAAGAAACCTCTCATCAGCTGTGTGTGACAAATGTCCT 228
QY 25 ProGlyThrPheValGlnArgProCysArgAspSerProThrThrCysGlyProCys 44
Db 229 CCTGGTACCTACCTAAACAACACTGTACAGCAAGTGGAGACCGGTGCGCCCTTGC 288
QY 45 ProProArgHisTyrThrGlnPheTrpAsnTyrLeuGluArgCysArgTyrCysAsnVal 64
Db 289 CCTGACCCTACTACACAGACAGCTGGCCACACCACTGACGAGTGTCTATACAGCCCC 348
QY 65 LeuCysGlyGluArgGluGluAlaArgAlaCysHisAlaThrHisAsnArgAlaCys 84
Db 349 GTGTGCAAGGAGTGCAGTACGTCACAGACAGTGCATCGACCCACACCCGCGTGTGC 408
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QY 125 ProProGlyThrPheSerAlaSerSerSerSerGluGlnCysGlnProHisArgAsn 144
Db 529 CCAGATGGGTCTCTCAATGAGACGTCATCTAAAGCACCTCTAAAGCACCCACACCAAT 588
QY 145 CysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerSerHisAspThrLeuCys 164
Db 589 TGCAGTGTCTTTTGTCTCTCTGCTAACTCAGAAAGGAAATGCAACACACGACACATA 645
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Db 646 -----TGTTCCGGAACAGTGAATCAACTCAAAATGTGGAATAGATGTTACCTGTGT 699

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Qy 183 GluArgAlaValIleAspPhe 189
Db 700 GAGGAGCATTCTCAGGTTT 720

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Pred. No.:	3,05e-26	Length:	1355
Score:	440.50	Matches:	77
Percent Similarity:	57.75%	Conservative:	31
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DB:	4	Gaps:	2

US-09-936-024-1 (1-271) X US-08-795-446B-5 (1-1355)

Oy 5 PRTHTYRPROTPARGASALGIUthrGlyluAglueValuAcySAlaGInCyPro 24
 Db 169 CCAAGTACCTTCATTATGACGAGAAACCTTCATCATGCGTGTGTGTGACAAATGTCT 222
 Oy 25 PROGIYthRheValGInARProCySaRgARgAsPeRProthThCySGLYProCys 44
 Db 229 CCTGTACTTACTTAACAACACCTGTACAGAAAGTGGAGACCCGTGTGGCCCCCTTGC 288
 Oy 45 PROPRoARghISYThrGlnhETrpAsnTYrleuGluARgCySaRgTYrCyAsnVal 64
 Db 289 CCTGACCACTACTACACAGACAGCTGGCACACAGATGACGAGTGTCTTACTGACGCC 348
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Qy 85 ArgCysArgThrGlyPhePheAlaIleAlaGlyPheCysLeuGluIleAlaSerCysPro 104

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Qy 105 ProGlyAlaGlyValIleAlaProGlyThrProSerGluAlaThrGlyIleCysGlnProCys 124

Db 469 CCTGGATTTGGAGTGGAGTGCAGCAAGCTGGAACCCAGAGCGAATATCAGTTTCCAAAGAATGT 528

Qy 125 ProProGlyThrPheSerAlaSerSerSerSerGluGlnCysGlnProIleAlaGln 144

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Qy 145 CysThrAlaLeuGlyLeuAlaAlaLeuAlaValProGlySerSerSerSerIleAspThrLeuCys 164

Db 589 TGCAGTGTCTTTGGTCTCTCTGCTACTACAGAAAGGAATCAACACACGCAACATAT 645

Qy 165 ThrSerCysThrGlyPheProLeuSerThrArgValProGlyAlaGluGlu-----Cys 182

Db 646 -----TGTTCGGGAAACAGTGAATCAACTCAAAATGTGAATGATGTTCACCTGTGT 699

Qy 183 GluArgAlaValIleAspPhe 189

Db 700 GAGGAGGCATTTCTCAGGTTT 720

RESULT 10

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US-08-706-945D-127
US-08-706-945D-127
Sequence 127, Application US/08706945D
Patent No. 6369027
GENERAL INFORMATION:
APPLICANT: Boyle, William
APPLICANT: Lacey, David
APPLICANT: Calzone, Frank
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: Osteoprotegerin
FILE REFERENCE: A-378CIP
CURRENT APPLICATION NUMBER: US/08/706,945D
CURRENT FILING DATE: 1996-09-03
Prior APPLICATION NUMBER: 08/577,788
Prior FILING DATE: 1995-12-22
NUMBER OF SEQ ID NOS: 145
SOFTWARE: PatentIn version 3.1
SEQ ID NO 127
LENGTH: 1355
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (94)..(1296)
OTHER INFORMATION:
US-08-706-945D-127

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Pred. No.:	3,056-26	Length:	1355
Score:	440.50	Matches:	77
Percent Similarity:	57.75%	Conservative:	31
Best Local Similarity:	41.1%	Mismatches:	74
Query Match:	29.5%	Indels:	5
DB:	4	Gaps:	2

US-09-936-024-1 (1-271) x US-08-706-945D-127 (1-1355)

Qy	5	ProthrrYrProTPrpAgaSgAlaGltThGlyGluYnrGueValCysAlaGlnCysPro	24
Db	169	CCAAGTACCTTATTTATGACGAAGAAACCTTCATCAGCTGTTGTGTGACAAATGCT	228
Qy	25	ProGlyIhrPheValGlnaGprProCysaGArGaSperProthrrThrCysGlyProCys	44
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Qy 65 LeuCysGlyGluArgGluGluAlaArgAlaCysHisAlaThrHisAsnArgAlaCys 84
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Db 349 GTGTGAAGGAGCTGCAGTACGTCAGCAGGAGTGCAATCGCACCAACCGGTGTC 408
      :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||
Qy 85 ArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHisAlaSerCysPro 104
      :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||
Db 409 GAATGCAAGGAAGCGGCTACCTTGATAGAGTCTGCTTGAACATAGAGTGCCT 468
      :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||
Qy 105 ProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGlnCysGlnProCys 124
      :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||
Db 469 CTTGGATTGGAGTGGGCGAAGCTGGAAACCCAGAGCGAATACAGTTTCAAAAAGATGT 528
      :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||
Qy 125 ProProGlyThrPheSerAlaSerSerSerGluGlnCysGlnProHisArgAsn 144
      :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||
Db 529 CCAGATGGGTCTTCTCAATGAGACGCTCATCTAAAGCACCCCTGTAGAAAACACACAAT 588
      :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||
Qy 145 CysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerSerHisAspThrLeuCys 164
      :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||
Db 589 TGCAGTCTCTTGTCTCTCTGCTAACTCAGAAAGGAATGCAACACACAGCAACATA--- 645
      :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||
Qy 165 ThrSerCysThrGlyPheProLeuSerThrArgValProGlyAlaGluGlu-----Cys 182
      :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||
Db 646 -----TGTTCCGGAAACAGTGAATCAACTCAAAATGTGGAATAGATGTTACCTGTGT 699
      :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||
Qy 183 GluArgAlaValIleAspPhe 189
      :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||
Db 700 GAGGAGCATCTTCAGGTTT 720
      :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||
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RESULT 11
US-08-997-918-47
; Sequence 47, Application US/08997918
; Patent No. 6077689
; GENERAL INFORMATION:
; APPLICANT: Snively, Marshall D.
; TITLE OF INVENTION: ENHANCED SOLUBILITY OF RECOMBINANT PROTEINS
; FILE REFERENCE: A-496
; CURRENT APPLICATION NUMBER: US/08/997,918
; CURRENT FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 47
; LENGTH: 525
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
; OTHER INFORMATION: fragment encoding amino acids 22-194 of human OPG
US-08-997-918-47
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Alignment Scores:
Pred. No.: 3,25e-26 Length: 525
Score: 433.00 Matches: 69
Percent Similarity: 60.87% Conservative: 29
Best Local Similarity: 42.86% Mismatches: 63
Query Match: 29.04% Indels: 0
DB: 3 Gaps: 0
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US-09-936-024-1 (1-271) x US-08-997-918-47 (1-525)
Qy 5 ProThrTyProTrpArgAspAlaGluThrGlyGluArgLeuValCysAlaGlnCysPro 24
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Db 16 CCTAAATATCTTATTATGATGAAGAACTAGTCACAGCTGCTGTCGCAAAATGCTCT 75
      :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||
Qy 25 ProGlyThrPheValGlnArgProCysArgAspSerProThrThrCysGlyProCys 44
      :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||
Db 76 CCGGTACCTACCTGAAACAGACTGCACCGCTAAATGGAACCCGTTTTCGCTCTCTGT 135
      :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||
Qy 45 ProProArgHisTyThrGlnPheThrAsnTyLeuGluArgCysArgTyCysAsnVal 64
      :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||
Db 136 CCGGACCACTACTACACCGACTCTCTGGCACACCTCGCAAAATGCTGACTGCTCACCG 195
      :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||
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Qy 65 LeuCysGlyGluArgGluGluAlaArgAlaCysHisAlaThrHisAsnArgAlaCys 84
      :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||
Db 196 GTTTGAAGGAGCTGCAGTACGTTAAACACAGGAATGCAACGTCACGCAACCGTGTATGC 255
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Qy 85 ArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHisAlaSerCysPro 104
      :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||
Db 256 GAATGCAAGGAAGGCTTACCTGAGATCGAATCTGCTGAAACACCCGTTCTCTGTCCG 315
      :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||
Qy 105 ProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGlnCysGlnProCys 124
      :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||
Db 316 CTTGGTTTCGGTGTCTACAGGCTGGTACCCCGAAGTAAACCGTTTGCACACCGTTGC 375
      :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||
Qy 125 ProProGlyThrPheSerAlaSerSerSerGluGlnCysGlnProHisArgAsn 144
      :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||
Db 376 CCGGACCGTTTCTTCTCAACGAAACCTCGAGCAAAAGCTCCGTCGCTAAACACACCAAC 435
      :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||
Qy 145 CysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerSerHisAspThrLeuCys 164
      :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||
Db 436 TGTCTCCGTTTTCGGTCTCTCTGTTAAACCCGAAAGGTACGTTACCCACGACATCTGC 495
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Qy 165 Thr 165
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Db 496 TCC 498
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RESULT 12
US-08-974-022-1
; Sequence 1, Application US/08974022
; Patent No. 6015938
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: OSTEOPROTEGERIN
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Dehaven Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,022
; FILING DATE: 12-DEC-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/577,788
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-378
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2432 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 124..1326
US-08-974-022-1

Alignment Scores:
Pred. No.: 1,06e-24 Length: 2432
Score: 425.50 Matches: 81
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Percent Similarity: 55.61% Conservative: 33
 Best Local Similarity: 39.51% Mismatches: 86
 Query Match: 28.54% Indels: 5
 DB: 3 Gaps: 2

US-09-936-024-1 (1-271) x US-08-974-022-1 (1-2432)

Qy 5 ProThrTyPrProTPrAaSPaAlaGluThrGluArgLeuValCysAlaGlnCysPro 24
 Db 199 CCAAAATACCTTGCATTATGAGCCGAGAAACCGAGACGCTCTTGTTGCAAAATGCT 258
 Qy 25 ProGlyThrPheValGlnArgProCysArgArgAspSerProThrThrCysGlyProCys 44
 Db 259 CCTGGCAGCTACCTAAACAGCACTGCACAGTCAGAGAGAACAGACAGTGTGCTCCCTGC 318
 Qy 45 ProProArgHisTyThrGlnPheThrPasnTyLeuGlnArgCysArgTyCysAsnVal 64
 Db 319 CCTGACTACTCTTATACAGACAGCTGCACAGATATGATGATGCTGACTGAGCCCC 378
 Qy 65 LeuCyseGlyGluArgGluGluGluAlaArgAlaCysHisAlaThrHisAsnArgAlaCys 84
 Db 379 GTGTGCAGAGAACTGCAGACCGGTAAACAGAGTGCAAACCCACCCACAGAGTGTGC 438
 Qy 85 ArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGlnHisAlaSerCysPro 104
 Db 439 GAATGTAGAGAAAGGCGCTACCTGAGCTCGAATTTGCTTGAAGCACCAGAGCTGTCCC 498
 Qy 105 ProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGlnCysGlnProCys 124
 Db 499 CCAGGCTTGGTGTGCTGCAGAGCTGGAGCCCAAGAGCAACAGGTTTGCMAAAAGATGT 558
 Qy 125 ProProGlyThrPheSerAlaSerSerSerSerSerGlnGlnCysGlnProHisArgAsn 144
 Db 559 CCGATGAGGTTCTTCTCAGAGTGAAGCTGATCGAAAGCAACCTGTAGAAACACACCAAC 618
 Qy 145 CysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerSerHisAspThrLeuCys 164
 Db 619 TGCAGCTCAGCTGCGCTCCTGCTATTCAGAAAGAAATGCAACACATGACAAATGTA--- 675
 Qy 165 ThrSerCysThrGlyPheProLeuSerThrArgValProGlyAlaGluGlu-----Cys 182
 Db 676 -----TGTTCCGGAACAGAGAAAGCACTCAAAATTTGTGAAATGATGTCACCCCTGTGC 729
 Qy 183 GluArgAlaValIleAspPheValAlaPheGlnAspIleSerIleLysArgLeuGlnArg 202
 Db 730 GAAGAGCATTTCTCAGGTTTCTGTGCTTACCAAGATTATACCAATGAGTGTGTT 789
 Qy 203 LeuLeuGlnAlaLeu 207
 Db 790 CTGGTGCAGAGTTTG 804
 RESULT 13
 US-08-795-445A-1
 : Sequence 1, Application US/08795445A
 : Patent No. 6284485
 : GENERAL INFORMATION:
 : APPLICANT: Boyle, William J.
 : APPLICANT: Lacey, David L.
 : APPLICANT: Calzone, Frank J.
 : APPLICANT: Chang, Ming-Shi
 : TITLE OF INVENTION: OSTEOPROTEGERIN
 : NUMBER OF SEQUENCES: 53
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Amgen Inc.
 : STREET: 1840 Dehavenland Drive
 : CITY: Thousand Oaks
 : STATE: California
 : COUNTRY: USA
 : ZIP: 91320-1789
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/795,445A
 : FILING DATE:
 : CLASSIFICATION:
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: 08/577,788
 : FILING DATE:
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Winter, Robert B.
 : REFERENCE/DOCKET NUMBER: A-378
 : INFORMATION FOR SEQ ID NO: 1:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 2432 base pairs
 : TYPE: nucleic acid
 : STRANDEDNESS: single
 : TOPOLOGY: linear
 : MOLECULE TYPE: cDNA
 : FEATURE:
 : NAME/KEY: CDS
 : LOCATION: 124..1326
 : US-08-795-445A-1

Alignment Scores:
 Pred. No.: 1,06e-24 Length: 2432
 Score: 425.50 Matches: 81
 Percent Similarity: 55.61% Conservative: 33
 Best Local Similarity: 39.51% Mismatches: 86
 Query Match: 28.54% Indels: 5
 DB: 4 Gaps: 2

US-09-936-024-1 (1-271) x US-08-795-445A-1 (1-2432)

Qy 5 ProThrTyPrProTPrAaSPaAlaGluThrGluArgLeuValCysAlaGlnCysPro 24
 Db 199 CCAAAATACCTTGCATTATGAGCCGAGAAACCGAGACGCTCTTGTTGCAAAATGCT 258
 Qy 25 ProGlyThrPheValGlnArgProCysArgArgAspSerProThrThrCysGlyProCys 44
 Db 259 CCTGGCAGCTACCTAAACAGCACTGCACAGTCAGAGAGAACAGACAGTGTGCTCCCTGC 318
 Qy 45 ProProArgHisTyThrGlnPheThrPasnTyLeuGlnArgCysArgTyCysAsnVal 64
 Db 319 CCTGACTACTCTTATACAGACAGCTGCACAGATATGATGATGCTGACTGAGCCCC 378
 Qy 65 LeuCyseGlyGluArgGluGluGluAlaArgAlaCysHisAlaThrHisAsnArgAlaCys 84
 Db 379 GTGTGCAGAGAACTGCAGACCGGTAAACAGAGTGCAAACCCACCCACAGAGTGTGC 438
 Qy 85 ArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGlnHisAlaSerCysPro 104
 Db 439 GAATGTAGAGAAAGGCGCTACCTGAGCTCGAATTTGCTTGAAGCACCAGAGCTGTCCC 498
 Qy 105 ProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGlnCysGlnProCys 124
 Db 499 CCAGGCTTGGTGTGCTGCAGAGCTGGAGACCCGAGAGGAACACGCTTGTGCAAAATGCT 558
 Qy 125 ProProGlyThrPheSerAlaSerSerSerSerSerGlnGlnCysGlnProHisArgAsn 144
 Db 559 CCGATGAGGTTCTTCTCAGGTGAGACGTCATCGAAAGCAACCTGTAGAGAAACACACCAAC 618
 Qy 145 CysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerSerSerHisAspThrLeuCys 164
 Db 619 TGCAGCTCAGCTGCGCTCCTGCTATTCAGAAAGAAATGCAACACATGACAAATGTA--- 675
 Qy 165 ThrSerCysThrGlyPheProLeuSerThrArgValProGlyAlaGluGlu-----Cys 182
 Db 676 -----TGTTCCGGAACAGAGAAAGCACTCAAAATTTGTGAAATGATGTCACCCCTGTGC 729
 Qy 183 GluArgAlaValIleAspPheValAlaPheGlnAspIleSerIleLysArgLeuGlnArg 202
 Db 730 GAAGAGCATTTCTCAGGTTTCTGTGCTTACCAAGATTATACCAATGAGTGTGTT 789

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QY 203 LeuLeuGlnAlaLeu 207
Db 790 CTGGTGACAGATTG 804

RESULT 14
US-08-795-447A-1
; Sequence 1, Application US/08795447A
; Patent No. 6284728
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: Osteoprotegerin
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: One Amgen Center Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91362-1789
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/795,447A
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-378D2
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2432 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 124..1326
US-08-795-447A-1

Alignment Scores:
Pred. No.: 1,06e-24 Length: 2432
Score: 425.50 Matches: 81
Percent Similarity: 55.61% Conservative: 33
Best Local Similarity: 39.51% Mismatches: 86
Query Match: 28.54% Indels: 5
DB: Gaps: 2

US-09-936-024-1 (1-271) x US-08-795-447A-1 (1-2432)

QY 5 ProThrTyrrProThrArgAspAlaGluThrGlyGluArgLeuValCysAlaGlnCysPro 24
Db 199 CCAAAATACCTTGATATGACCCAGAAACCGAGCTCTTGTTGTGACAAATGTGCT 258
QY 25 ProGlyThrPheValGlnArgProCysArgAspSerProThrThrCysGlyProCys 44
Db 259 CCTGGCACTTACCTAAACAGCACTGCACAGTCAGGAGGAGACACTGTGTGCTCCCTTGC 318
QY 45 ProProArgHisThrThrGlnPheThrAsnTyrrLeuGluArgCysArgTyrrCysAsnVal 64
Db 319 CCTGACTACTCTTATACAGACAGCTGGCCACAGAGTGAATGCGTGTACTGCAGCCCC 378
QY 65 LeuCysGlyGluArgGluGluAlaArgAlaCysHisAlaThrHisAsnArgAlaCys 84
Db 379 GTGTGCAAGAACTGACAGACCGGTGAACAGAGGTGCAACCGCACCCACACCGAGTGTGC 438
QY 85 ArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHisAlaSerCysPro 104

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Db 439 GAATGTGAGGAGGGCGCTACCTGGAGCTCGAATCTGCTTGAAGCACCGGAGCTGTCCC 498
QY 105 ProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGlnCysGlnProCys 124
Db 499 CCAGGCTTGGGTGTGCTGCAGGCTGGGACCCAGAGCGAAACACCGTTTGCAGAAAGATGT 558
QY 125 ProProGlyThrPheSerAlaSerSerSerSerGluGlnCysGlnProHisArgAsn 144
Db 559 CCGGATGGGTCTTCTCAGGTGAGACGTCATCGAAAGACACCCCTGTAGGAAACACACCAAC 618
QY 145 CysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerSerHisAspThrLeuCys 164
Db 619 TGAGCTCACTTGGCTCTCTGCTAATTGAGAAAGAAATGCAACACATGACAATGTA--- 675
QY 165 ThrSerCysThrGlyPheProLeuSerThrArgValProGlyAlaGluGlu-----Cys 182
Db 676 -----TGTTCCGGAACAGAGNAGCACTCAAAATTGTGGAATAGATGTACCCTGTGC 729
QY 183 GluArgAlaValIleAspPheValAlaPheGlnAspIleSerIleLysArgLeuGlnArg 202
Db 730 GAAGAGGCATTCTTCAGGTTCGTGTGCTGCTACCAAGATTATACCGAATTGCTGAGTGT 789
QY 203 LeuLeuGlnAlaLeu 207
Db 790 CTGGTGACAGATTG 804

RESULT 15
US-08-974-186-1
; Sequence 1, Application US/08974186
; Patent No. 6284740
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: OSTEOPROTEGERIN
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,186
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/577,788
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-378
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2432 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 124..1326
US-08-974-186-1

Alignment Scores:

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GenCore version 5.1.3
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Run on: January 6, 2003, 11:31:16 ; Search time 132 Seconds
(without alignments)
887.945 Million cell1 updates/sec

Title: US-09-936-024-1
Perfect score: 1491
Sequence: 1 VAEPTPYPMRDATGRLVC.....RVAMPGLRSYRERLPVH 271

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 381593 segs, 216252194 residues
Total number of hits satisfying chosen parameters: 763186

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-Q=/cgn2_1/USFTO.spool/US09936024/runat_06012003_111608_12202/app_query.fasta_1.455
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-LOOPCL=0 -LOOPEXT=0 -UNITS=bites -START=1 -END=1 -MATRIX=blosum62
-TRANS-human40.csl -LIST=45 -DOCLALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US09936024@cgn 1.1 33 @runat_06012003_111608_12202
-NCPU=6 -ICPU=3 -NO_XLPHY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications NA:*

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- 3: /cgn2_6/prodata/2/pubpna/US06_NEW_PUB.seq:*
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- 6: /cgn2_6/prodata/2/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/prodata/2/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/prodata/2/pubpna/US08_PUBCOMB.seq:*
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- 11: /cgn2_6/prodata/2/pubpna/US10_NEW_PUB.seq:*
- 12: /cgn2_6/prodata/2/pubpna/US10_PUBCOMB.seq:*
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- 14: /cgn2_6/prodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	1491	100.0	1077	10	US-09-935-727-1
3	1491	100.0	1114	10	US-09-896-096A-2
4	1491	100.0	1114	10	US-09-894-924-2

5	1491	100.0	1347	10	US-09-877-156-18	Sequence 18, Appl
6	1491	100.0	1550	10	US-09-935-727-33	Sequence 33, Appl
7	1469	98.5	1137	10	US-09-840-795-1	Sequence 1, Appl
8	1339	89.8	1859	10	US-09-877-156-19	Sequence 19, Appl
9	1287.5	86.4	1796	10	US-09-935-727-28	Sequence 28, Appl
10	982.5	65.9	1667	10	US-09-935-727-3	Sequence 3, Appl
11	858	57.5	491	10	US-09-896-096A-3	Sequence 3, Appl
12	858	57.5	491	10	US-09-894-924-3	Sequence 3, Appl
13	841	56.4	459	10	US-09-877-156-7	Sequence 7, Appl
14	461	30.9	981	10	US-09-062-113-92	Sequence 92, Appl
15	442.5	29.7	1206	10	US-09-062-113-83	Sequence 83, Appl
16	440.5	29.5	819	10	US-09-062-113-96	Sequence 96, Appl
17	440.5	29.5	966	10	US-09-062-113-101	Sequence 101, Appl
18	440.5	29.5	984	10	US-09-062-113-93	Sequence 93, Appl
19	440.5	29.5	1056	10	US-09-062-113-95	Sequence 95, Appl
20	440.5	29.5	1089	10	US-09-062-113-10	Sequence 10, Appl
21	440.5	29.5	1182	10	US-09-062-113-100	Sequence 100, Appl
22	440.5	29.5	1200	10	US-09-062-113-94	Sequence 94, Appl
23	440.5	29.5	1203	12	US-10-105-934-3	Sequence 3, Appl
24	440.5	29.5	1206	10	US-09-062-113-6	Sequence 6, Appl
25	440.5	29.5	1206	10	US-09-062-113-85	Sequence 85, Appl
26	440.5	29.5	1206	10	US-09-062-113-86	Sequence 86, Appl
27	440.5	29.5	1206	10	US-09-062-113-87	Sequence 87, Appl
28	440.5	29.5	1356	10	US-09-954-456-1164	Sequence 1164, Appl
29	440.5	29.5	1527	12	US-10-164-592-1	Sequence 1, Appl
30	440.5	29.5	2122	12	US-10-105-934-14	Sequence 14, Appl
31	440.5	29.5	2133	12	US-10-105-934-1	Sequence 1, Appl
32	440.5	29.5	2139	10	US-09-765-231A-4	Sequence 4, Appl
33	433.5	29.1	1206	10	US-09-062-113-84	Sequence 84, Appl
34	433	29.0	564	10	US-09-062-113-102	Sequence 102, Appl
35	433	29.0	594	10	US-09-062-113-97	Sequence 97, Appl
36	432	29.0	1185	10	US-09-062-113-8	Sequence 8, Appl
37	424	28.4	271	10	US-09-896-096A-5	Sequence 5, Appl
38	424	28.4	271	10	US-09-894-924-5	Sequence 5, Appl
39	423	28.4	263	10	US-09-896-096A-10	Sequence 10, Appl
40	423	28.4	283	10	US-09-894-924-10	Sequence 10, Appl
41	384	25.8	201	10	US-09-896-096A-6	Sequence 6, Appl
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43	380	25.5	499	10	US-09-935-727-17	Sequence 17, Appl
44	365	24.5	226	10	US-09-896-096A-9	Sequence 9, Appl
45	365	24.5	226	10	US-09-894-924-9	Sequence 9, Appl

ALIGNMENTS

RESULT 1
US-09-935-727-32
; Sequence 32, Application US/09935727
; Patent No. US20020150583A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Tumor Necrosis Factor Receptors 6 Alpha and 6 Beta
; FILE REFERENCE: PP454P2
; CURRENT APPLICATION NUMBER: US/09/935,727
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/303,224
; PRIOR FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: 60/252,131
; PRIOR FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: 60/227,598
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: 09/518,931
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: 60/168,235
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: 60/146,371
; PRIOR FILING DATE: 1999-08-02
; PRIOR APPLICATION NUMBER: 60/131,964
; PRIOR FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: 60/131,270
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/124,092
; PRIOR FILING DATE: 1999-03-12

Qv 41 CvsGlvP

Db	232	TGTGGCCCGCTGTCCACCGCGGCACCTACACGCGAGTTCTGGAACTACCTGGAGCGCTGGCCG	291
Qy	61	TYTCYSANVALEUCYSGLYGUAARGLUGLUGLUALAARGALACYSHISALATHHIS	80
Db	292	TACTGCACACGCTCTCTGGGGAGACGCTGAGAGAGAGGACACGGGCTTCCACGCCACCCAC	351
Qy	81	ASNAARGALACYSARGCYSGARTGHDLYPHEPHELAHISALAGLYPHECYGLEUJNHIS	100
Db	352	AACCGTGCTCCCGCTGGCGGACCGGCTTCTTGGCGCACGCTGGATTTCTGTTGGACAC	411
Qy	101	ALASERCYSPPROGLYALAGLYVALIILEAPPROGLYTHRPROSERGLNASTHGLN	120
Db	412	GCATCTGTCTCACCTGTGGGCGGGGTGATTTCCCGGGACACCCCAAGCAGAACACGAC	471
Qy	121	CYSGLNPROCYSPROPROGLYTHRPHESERGLASERSESRSESRGJUGLINCYSGLN	140
Db	472	TGCAGCGGTCGCCGCCGAGCACCTTCTCAGCCAGACAGCTCAGACTCAGAGCAGTGCCAG	531
Qy	141	PROHISARGANCYSITHRALALEUGLYLEUALALEUENVALPROGLYSESRSESRHIS	160
Db	532	CCCCACGGCACTCACGCGCCCTGGCGCTGGCCCTCAATGCGCAGGCTTCTCCCTCCAT	591
Qy	161	ASPHRILEUCYSTRHSERCYSTHSGLYPHEPROLEUSERTHRAGVALPROGLYALAGLU	180
Db	592	GACACCTCTGTACACAGCTGCAGCTGGCTTCCCCCTCAGACACAGAGGTACAGAGACTGAG	651
Qy	181	GLUCYSGIARGALAVALLIILEASPHEVALALAPHEGLNAPLIESERILEYSARGLEU	200
Db	652	GAGTGTGAGCGGTGCGTCATGACTTTGTGGCTTTCCAGGACATCTCATCAAGAGCTG	711
Qy	201	GLNARGLEUENGLNALALEUGLUALAPROGLUGLYTPRGLYPROTHPRORAGLALGLY	220
Db	712	CAGCGGTGCTGCAGCGCCCTTCGAGCGCCCGAGGCTGGGGGTCCGACACCAAGGCCGCGC	771
Qy	221	ARGVALALEUGLNULEUYSLEUARGARGHLEUTHRGULIEULEUGLYALAGLNASP	240
Db	772	CGCGGGCTTTCAGACTGAGACTGTGTGGGGGCTCAGGGAGCTCTGGGGGCCAGAGAC	831
Qy	241	GLYVALLEUENVALARGLEULEUGLNALALEUARGVALALAAETMETPROGLYLEUGLU	260
Db	832	GGGGCGCTGCTGGTGGCGCTCTCTCAGAGCGCTGGCGCGTGGCAGAGATGCCGGGCTGAG	891
Qy	261	ARGSERVALARGIUAARGPHELEUPROVALHIS	271
Db	892	CGGAGCGTCCGTGAGCGCTTCTCCCTGTGCAC	924
RESULT 3			
US-09-896-096A-2			
Sequence 2, Application US/09896096A			
Patent No. US2002006159A1			
GENERAL INFORMATION:			
APPLICANT: ASHKENAZI, AVI J			
APPLICANT: BOTSSTEIN, DAVID			
APPLICANT: DODGE, KELLY H.			
APPLICANT: GURNEY, AUSTIN L.			
APPLICANT: KIM, KYUNG JIN			
APPLICANT: LAWRENCE, DAVID A.			
APPLICANT: PITTI, ROBERT			
APPLICANT: ROY, MARGARET A			
APPLICANT: TOMAS, DANIEL B			
APPLICANT: WOOD, WILLIAM I.			
TITLE OF INVENTION: DCR3 Polypeptide, A TNFR Homolog			
FILE REFERENCE: P134R2 REVISED			
CURRENT APPLICATION NUMBER: US/09/896,096A			
CURRENT FILING DATE: 2001-06-28			
PRIOR APPLICATION NUMBER: US 09/157,289			
PRIOR FILING DATE: 1998-09-18			
PRIOR APPLICATION NUMBER: US 60/059,288			
PRIOR FILING DATE: 1997-09-18			
PRIOR APPLICATION NUMBER: US 60/094,640			
PRIOR FILING DATE: 1998-07-30			
NUMBER OF SEQ ID NOS: 18			

[illegible]

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US-09-894-924-2
; Sequence 2, Application US/09894924
; Patent No. US20020065210A1
; GENERAL INFORMATION:
; APPLICANT: ASHKENAZI, AVI J
; APPLICANT: BOTSTEIN, DAVID
; APPLICANT: DODGE, KELLY H.
; APPLICANT: GURNEY, AUSTIN L.
; APPLICANT: KIM, KYUNG JIN
; APPLICANT: LAWRENCE, DAVID A.
; APPLICANT: PITTI, ROBERT
; APPLICANT: ROY, MARGARET A
; APPLICANT: TUMAS, DANIEL B
; APPLICANT: WOOD, WILLIAM I.
; TITLE OF INVENTION: DCR3 Polypeptide, A TNFR Homolog
; FILE REFERENCE: P1134R2 REVISED
; CURRENT APPLICATION NUMBER: US/09/894,924
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US 09/157,289
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: US 60/059,288
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: US 60/094,640
; PRIOR FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 18
; SEQ ID NO 2
; LENGTH: 1114
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: Unsure
; LOCATION: 1090
; OTHER INFORMATION: Unknown base
; US-09-894-924-2

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Pred. No.:	4.15e-106
Score:	1491.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	100.00%
DB:	10
Length:	1114
Matches:	271
Conservative:	0
Mismatches:	0
Indels:	0
Gaps:	0

US-09-936-024-1 (1-271) x US-09-894-924-2 (1-1114)

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Db	188	G	T	G	G	C	A	G	A	A	A	C	C	C	A	C	T	T	A	C	C	T	G	G	C	G	G	A	C	G	A	G	A	C	A	G	A	C	A	G	G	G	A	C	G	G	T	G	T	G	T	G	C	247							
Qy	21	A	l	a	G	l	n	C	y	s	P	r	o	G	l	y	T	h	r	P	h	e	V	a	l	G	l	n	A	r	g	P	r	o	C	y	s	A	r	g	A	s	p	S	e	r	P	r	o	T	h	r	40								
Db	248	G	C	C	A	G	T	G	C	C	C	C	A	G	C	A	C	T	T	T	G	T	G	C	A	G	C	G	C	G	T	G	C	C	G	C	G	A	C	A	G	C	C	C	C	A	G	C	A	G	307										
Qy	41	C	y	s	G	l	y	P	r	o	C	y	s	P	r	o	A	r	g	H	i	s	T	y	r	T	h	r	G	l	n	P	h	e	T	r	p	A	s	n	T	y	r	l	e	u	A	r	g	C	y	s	A	r	g	60					
Db	308	T	G	T	G	G	C	C	C	G	T	C	A	C	G	C	G	C	C	A	C	A	C	G	C	A	G	C	A	G	C	A	G	C	A	G	T	T	C	G	A	A	C	T	G	A	C	T	G	A	G	C	G	C	367						
Qy	61	T	y	r	C	y	s	A	s	n	V	a	l	L	e	u	C	y	s	G	l	y	A	r	g	G	l	u	G	l	u	A	l	a	A	r	g	A	l	a	C	y	s	H	i	s	A	l	a	T	h	r	H	i	s	80					
Db	368	T	A	C	T	G	A	C	A	C	G	T	C	T	T	G	C	G	G	G	A	G	C	T	G	A	G	A	G	A	G	A	G	A	G	A	G	A	G	A	G	A	G	A	G	A	G	A	G	A	G	427									
Qy	81	A	s	n	A	r	g	A	l	a	C	y	s	A	r	g	C	y	s	A	r	g	T	h	r	G	l	y	P	h	e	P	h	e	A	l	a	H	i	s	A	l	a	G	l	y	P	h	e	C	y	s	L	e	u	H	i	s	100		
Db	428	A	A	C	G	T	G	C	T	G	C	C	G	C	A	C	C	G	C	T	C	T	T	C	G	C	A	C	C	G	C	A	C	C	G	C	A	C	C	G	C	T	G	T	G	A	G	A	C	487											
Qy	101	A	l	a	S	e	r	C	y	s	P	r	o	G	l	y	A	l	a	G	l	y	V	a	l	L	e	a	A	p	r	o	G	l	y	T	h	r	P	r	o	S	e	r	G	l	n	A	n	T	h	r	G	l	n	120					
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Qy	121	CysGlnProCysProGlyThrPheSerAlaSerSerSerGluGlnCysGln	140
Db	548	TGCAGAGCGTGCCTCCAGGAGCCTTCTCAGCCAGAGCTCCAGCTCAGAGCAGTCCCGAG	607
Qy	141	ProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerSerHis	160
Db	608	CCCACCGCAACTGCACGGCCCTGGGGCTGGCCCTCAATGTGCCAGGCTCTTCTCCCTCAT	667
Qy	161	AspThrLeuCysThrSerCysThrGlyPheProLeuSerThrArgValProGlyAlaGlu	180
Db	668	GACACCTGTGCACCAAGCTGCACCTGGCTTCCCTCAGCACCAAGGCTACCAAGAGCTGAG	727
Qy	181	GluCysGluArgAlaValIleAspPheValAlaPheGlnAspIleSerIleYsArgLeu	200
Db	728	GAGTGTGAGCGTGCCTGCATCGACTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG	787
Qy	201	GlnArgLeuLeuGlnAlaLeuGluAlaProGluGlyTyrGlyProThrProArgAlaGly	220
Db	788	CAGCGGTGTGTGAGGCCCTCGAGGCCCGAGGGCTGGGGTCCGACACCAAGGGCGGGC	847
Qy	221	ArgAlaAlaLeuGlnLeuLysLeuArgArgLeuThrGluLeuLeuGlyAlaGlnAsp	240
Db	848	CGCGCGGCGCTTGCAGCTGAAAGTGCCTGGCGGCTCACAGAGCTCTCGGGGCGCAGGAC	907
Qy	241	GlyAlaLeuLeuValArgLeuLeuGlnAlaLeuArgValAlaArgMetProGlyLeuGlu	260
Db	908	GGGCGCTGTGTGGTGGCGTGTGTGAGGCCCTCGCGGTGCCAGGATGCCCGGGCTGGAG	967
Qy	261	ArgSerValArgGluArgPheLeuProValHis	271
Db	968	CGGAGCGTCCGTGAGCGCTTCTCCCTGTGCAC	1000

RESULTS

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RES001.5
US-09-877-156-18
; Sequence 18, Application US/09877156
; Patent NO. US20020055625A1
; GENERAL INFORMATION:
; APPLICANT: Catherine Tribouley
; TITLE OF INVENTION: NEW MEMBERS OF TNF AND TNFR FAMILIES
; FILE REFERENCE: 1408.003/200130.439C1
; CURRENT APPLICATION NUMBER: US/09/877,156
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 09/286,529
; PRIOR FILING DATE: 1998-04-05
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Fast-SEQ for Windows Version 3.0
; SEQ ID NO 18
; LENGTH: 1347
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-877-156-18

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Alignment Scores:		
Pred. No.:	5, 21e-106	Length:
Score:	1491.00	Matches:
Percent Similarity:	100.00%	Conservative:
Best Local Similarity:	100.00%	Mismatches:
Query Match:	100.00%	Indels:
DB:	10	Gaps:

US-09-936-024-1 (1-271) x US-09-877-156-18 (1-1347)

Qy	1	ValAlaGluThrProThrTyrProThrArgAspAlaGluThrGlyGluArgLeuValCys	20
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Qy	21	AlaGlnCysProGlyThrPheValGlnArgProCysArgArgAspSerProThrThr	40
Db	465	GCCGAGTGCCCCAGGACCTTTGTGAGGGCCGTGCGCGGACAGCCCCAGCAGC	524
Qy	41	CysGlyProCysProArgHisTyrThrGlnPheTrpAsnTyrLeuGluArgCysArg	60
Db	525	TGTGGCCGGTGTCCACGGGCCACTACAGCAGTTCTGGAATCTCTGAGGCGCTCCGC	584

QY 241 GlyAlaLeuValArgLeuLeuGlnAlaLeuArgValAlaArgMetProGlyLeuGlu 260
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Db 1458 GGTGCTTGTGTAGATTGTTGCAAGCTTTGAGAGTTTGTAGATTGCTGTTGGAA 1517
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QY 261 ArgSerValArgGluArgPheLeuProValHis 271
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Db 1518 AGATCTGTTAGAAAGATTTTGGCCAGTTTCC 1550
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RESULT 7
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; Sequence 1, Application US/09840795
; Patent No. US20020143147A1
; GENERAL INFORMATION:
; APPLICANT: Murphy, Erin E.
; APPLICANT: Mattson, Jeanine D.
; APPLICANT: Bates, Elizabeth Esther Mary
; APPLICANT: Gorman, Daniel M.
; APPLICANT: Lebecque, Serge J.E.
; TITLE OF INVENTION: Mammalian Genes; Related Reagents
; FILE REFERENCE: SF0818K
; CURRENT APPLICATION NUMBER: US/09/840,795
; CURRENT FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: 09/351,777
; PRIOR FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1137
; TYPE: DNA
; ORGANISM: primate
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (99)..(998)
; NAME/KEY: misc feature
; LOCATION: (367)
; OTHER INFORMATION: W; may be A or T
; NAME/KEY: mat_peptide
; LOCATION: (132)..(998)
US-09-840-795-1
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Pred. No.: 2,06e-104 Length: 1137
Score: 1469.00 Matches: 268
Percent Similarity: 98.89% Conservative: 0
Best Local Similarity: 98.89% Mismatches: 3
Query Match: 98.52% Indels: 0
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Db 186 GTGGCAGAAACCCACCTACCTCCCTGGCGGAGCGCAGACAGGGGAGCGGCTGGTGTGC 245
|
QY 21 AlaGlnCysProGlyThrPheValGluArgProCysArgArgAspSerProThrThr 40
|
Db 246 GCCCAGTGGCCCCCAGGACCTTTGTGACGGCGGTGGCGGAGACAGCCCGCATGACG 305
|
QY 41 CysGlyProCysProProArgHisTyroThrGlnPheTrpAsnTyroLeuGluArgCysArg 60
|
Db 306 TGTGGCCCGGTGTCACCGCGCCCACTACACGAGTTCTGGAACTACCTGGAGCGGTGCGC 365
|
QY 61 TyrCysAsnValLeuCysGlyGluArgGluGluAlaArgAlaCysHisAlaThrHis 80
|
Db 366 TWCTGTACGTCTCTCGGGGAGCGTGGAGGAGGACAGCGGCTTGCACGCCACCCAC 425
|
QY 81 AsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHis 100
|
Db 426 AACCGTGCCTGCCGCTGCCGACCGGCTTCTTCGCGACGCTGGTTCTGCTTGGAGCAC 485
|
QY 101 AlaSerCysProProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGln 120
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Db 486 GCATCGTGTCCACCTGGTGGCGGCGTGATTGCCCGGGCACCCCGAGCAGAACACGCAG 545
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QY 121 CysGlnProCysProProGlyThrPheSerAlaSerSerSerSerGluGlnCysGln 140
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QY 161 AspThrLeuCysThrSerCysThrGlyPheProLeuSerThrArgValProGlyAlaGlu 180
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Db 666 GACACCTCTGTCACAGCTGCTGCTTCCCTCCAGCAGGAGTACAGGAGCTGAG 725
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QY 181 GluCysGluArgAlaValIleAspPheValAlaPheGlnAspIleSerIleCysArgLeu 200
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QY 201 GlnArgLeuGlnAlaLeuGluAlaProGluGlyTrpGlyProThrProArgAlaGly 220
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Db 786 CAGCGGCTGCTGACGCGCTTCGAGGCGCCGAGGGGCTGGGTCGACACCAAGGGCGGGC 845
|
QY 221 ArgAlaAlaLeuGlnLeuLysLeuArgArgLeuThrGluLeuGlyAlaGlnAsp 240
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Db 846 CCGCGGCGCTTGCAGCTGAAGCTGCGTGGCGGCTCAGGAGCTCTGGGGGCGCAGGAC 905
|
QY 241 GlyAlaLeuValArgLeuGlnAlaLeuArgValAlaArgMetProGlyLeuGlu 260
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Db 906 GGGGCGCTGCTGTCGGCTGCTGACGCGCTGCGCGCTGGCGAGGATGCCCGGCTGGAG 965
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QY 261 ArgSerValArgGluArgPheLeuProValHis 271
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Db 966 CGGAGCGTCCGTGAGCGCTTCTCCCTGTGCAC 998
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RESULT 8
US-09-877-156-19
; Sequence 19, Application US/09877156
; Patent No. US2002005625A1
; GENERAL INFORMATION:
; APPLICANT: Catherine Tribouley
; TITLE OF INVENTION: NEW MEMBERS OF TNF AND TNFR FAMILIES
; FILE REFERENCE: 1408.003/200130.439C1
; CURRENT APPLICATION NUMBER: US/09/877,156
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 09/286,529
; PRIOR FILING DATE: 1998-04-05
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 1859
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-877-156-19
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Pred. No.: 3,37e-94 Length: 1859
Score: 1339.00 Matches: 271
Percent Similarity: 51.72% Conservative: 0
Best Local Similarity: 51.72% Mismatches: 0
Query Match: 89.81% Indels: 253
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Db 165 GTGGCAGAAACCCACCTACCTCCCTGGCGGAGCGCAGACAGGGGAGCGGCTGGTGTGC 224
|
QY 21 AlaGlnCysProGlyThrPheValGlnArgProCysArgArgAspSerProThrThr 40
|
Db 225 GCCCAGTGGCCCCCAGGACCTTTGTGACGGCGCTGGCGGCGGAGCAGCCCGACG 284
|
QY 41 CysGlyProCysProProArgHisTyroThrGlnPheTrpAsnTyroLeuGluArgCysArg 60
|

Db 285 TGTGCCCCGTGTCACCGCGCCACTACACGAGTTCTGGAACTACTGAGAGCGTCCGC 344
Qy 61 TTTCTAaenValleuCyGylYgluArggluGluAlaArgAlaCyHisAlaThrHis 80
Db 345 TACTGCAACGCTCTCTGCGGGAGGCTGAGAGAGGACCGGCTTGGCCAGCCACCA 404
Qy 81 AsnArgAlaCyArgCyArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHis 100
Db 405 AACGGTGGCTCCGCTGCGCACCGGCTTCTTCCGCGCACGGTGGTTCTGCTGGAGCAC 464
Qy 101 AlaSerCyProProGlyAlaGlyValIleAlaProGlyThrProSerGluAsnThrGln 120
Db 465 GCATCTGTGTCCACCTGAGTCCGCGCTGATGCTCCGCGCACCCCGACAGAACACGCGAG 524
Qy 121 CysGlnProCyProProGlyYThrPheSerAlaSerSerSerSerSerGluGlnCysGln 140
Db 525 TGCCAGCGCTGCCCCCGACGACCTTCTCAAGCCAGACGCTCCAGCTTCAGAGCAGTCCAG 584
Qy 141 ProHisArgAenCySerThrAlaLeuGlyLeuAlaLeuAenValProGlySerSerSerHis 160
Db 585 CCCACCGCAACTGACGCGCTGCGGCTGCGCTCATATGTCAGAGCTCTTCCCTCCCAT 644
Qy 161 AspThrLeuCySerThrSerCySerThrGlyPheProLeuSerThrArgValPro----- 177
Db 645 GACACCCCTGTACACAGCTGACGTGCTTCCCTCCACAGCAGGAGTACAGAGTACCA 704
Qy 177 ----- 177
Db 705 GAGGCTGAGGGGAGACACACTGACAGGCCACCTTGTGCTTGTCTGCTGCTTCCCT 764
Qy 177 ----- 177
Db 765 GCAGGTGATCTAGAGCTGAGGAGTCCAGTGGCTCTGGAAAGGGGCCACAGTGGATTGG 824
Qy 177 ----- 177
Db 825 AGGGGTGAGGGGTCCCTCCACTAGATCCCAACAAGTCTGCCCTCTCAGGGGTGGCTGAG 884
Qy 177 ----- 177
Db 885 AATTGTGATCTGAGCCAGGAGGACAGCTCCCTCGAGAGCTCTGGGAAAGTGGGACGAA 944
Qy 177 ----- 177
Db 945 TCTCTAAGTCCCGAGGGGAAAGTGGCTGCTCTGACACGCGGGAACCGAGGCTG 1004
Qy 177 ----- 177
Db 1005 ATGTAAATTCTCTAACTGCTGAGAGGAAAGTGGCTGCTCTCTGACATGGGAAACC 1064
Qy 177 ----- 177
Db 1065 GAGGCCAATGTAACTGCTGTGAGAAAGTACAGAGGGGAAAGTACCCCTTAAATCA 1124
Qy 177 ----- 177
Db 1125 GTCAAGTCCGCTCATCTGACAGTCCCACTGCCCCCTTCCGATGGCCAGAGGCCCAA 1184
Qy 177 ----- 177
Db 1185 GCCCTGTGCGGGCCCCCTTGTCTTGGACCAAGGTCGAGTGGCGGCTCTGCCCCC 1244
Qy 177 ----- 177
Db 1245 TAGGCTTTGCTCCAGCTCTTGAACGAAGGCTCTGCCCCCTTCCAGTCCCATGCTT 1304
Qy 177 ----- 177
Db 1305 GCACGTGCTCTCCAGACGAGGCTCAGCAGAGGATTTCTCTCTCTGCAAAACCCCGG 1364
Qy 177 ----- 177

Db 1365 AGTGGGGCCAGAAAGAGGTACTGTGACAGCCCCCGCACGTGTGTGTGGTGAATGAT 1424
Qy 178 -----GlyAlaGluGluCysGluArgAlaValIleAs 188
Db 1425 CGGACCGCTGCTCCCAACCCACTGACAGAGCTGAGAGGTGAAGGTGCTGCTCATCGA 1484
Qy 188 pPheValAlaPheGlnAspIleSerIleLeuArgLeuGlnArgLeuGlnAlaLeuG 208
Db 1485 CTTGTGGCTTCCAGGACATCTCATCAAGAGCTCAGCGGCTGCTGACAGGCTCTGCA 1544
Qy 208 uAlaProGlyYThrGlyProThrProAlaGlyAlaArgAlaAlaLeuGlnLeuGly 228
Db 1545 GGGCCCGAGGGCTGGGGTCCGACACCAAGGCGCGGCTTGGCAGCTGAAGCT 1604
Qy 228 uArgArgArgLeuThrGluLeuLeuGlyValAlaAspGlyValaLeuLeuValaArgLeu 248
Db 1605 GCGTCGGCGGCTTCCAGAGCTCTTGGGAGGCGACAGAGGCGGCTGCTGAGCGGCTGCT 1664
Qy 248 uGlnAlaLeuArgValAlaArgMetProGlyLeuGluArgSerValaArgGluArgPhe 268
Db 1665 GCAGGCGGTGCGGCTGCGACAGATGCCCGGCTGAGCGGAGCGTCCGTAGCGCTTCT 1724
Qy 268 uProValHis 271
Db 1725 CCTGTGTCAC 1734

RESULT 9
US-09-935-727-28
Sequence 28, Application US/09935727
Patent No. US20020150583A1
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Tumor Necrosis Factor Receptors 6 Alpha and 6 Beta
FILE REFERENCE: PR454P2
CURRENT APPLICATION NUMBER: US/09/935,727
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: 60/303,224
PRIOR FILING DATE: 2001-07-06
PRIOR APPLICATION NUMBER: 60/252,131
PRIOR FILING DATE: 2000-11-21
PRIOR APPLICATION NUMBER: 60/227,598
PRIOR FILING DATE: 2000-08-25
PRIOR APPLICATION NUMBER: 09/518,931
PRIOR FILING DATE: 2000-03-03
PRIOR APPLICATION NUMBER: 60/168,235
PRIOR FILING DATE: 1999-12-01
PRIOR APPLICATION NUMBER: 60/146,371
PRIOR FILING DATE: 1999-08-02
PRIOR APPLICATION NUMBER: 60/131,964
PRIOR FILING DATE: 1999-04-30
PRIOR APPLICATION NUMBER: 60/131,270
PRIOR FILING DATE: 1999-04-27
PRIOR APPLICATION NUMBER: 60/124,092
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/121,774
PRIOR FILING DATE: 1999-03-04
PRIOR APPLICATION NUMBER: 09/006,352
PRIOR FILING DATE: 1998-01-13
PRIOR APPLICATION NUMBER: 60/035,496
PRIOR FILING DATE: 1997-01-14
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 28
LENGTH: 1796
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: intron
LOCATION: 425-560
NAME/KEY: intron
LOCATION: 756-1512
US-09-935-727-28

Alignment Scores:

Pedigree No.: 2.85e-90	Length:	1790
Score: 1287.50	Matches:	271
Percent Similarity: 47.54%	Conservative:	0
Best Local Similarity: 47.54%	Mismatches:	0
Query Match: 86.33%	Indels:	299
DB: 10	Gaps:	2

US-09-936-024-1 (1-271) x US-09-935-727-28 (1-1796)

[illegible]

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; PRIOR APPLICATION NUMBER: 60/146,371
; PRIOR FILING DATE: 1999-08-02
; PRIOR APPLICATION NUMBER: 60/131,964
; PRIOR FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: 60/131,270
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/124,092
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/121,774
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: 09/006,352
; PRIOR FILING DATE: 1998-01-13
; PRIOR APPLICATION NUMBER: 60/035,496
; PRIOR FILING DATE: 1997-01-14
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 1667
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (73)..(582)
US-09-935-727-3

Alignment Scores:
Pred. No.: 6e-67 Length: 1667
Score: 982.50 Matches: 179
Percent Similarity: 78.85% Conservative: 0
Best Local Similarity: 78.85% Mismatches: 2
Query Match: 65.90% Indels: 46
Gaps: 1

US-09-936-024-1 (1-271) x US-09-935-727-3 (1-1667)
QY 1 ValAlaGluThrProThrTyrProTrrPaRgaApaAgluThnglyGluArgLeuValCys 20
Db 160 GTGGAGAAACACCACTACCCCTGGCGGAGCGAGACAGAGGAGGAGCGGCTGGTGGC 219
QY 21 AlaGlnCysProProGlyThrPheValGlnArgProCysArgArgSerProThrThr 40
Db 220 GCCCAGTGGCCCCCAGGACCTTGTGTGAGCGCGCTGCCGCCAGACAGCCCAACGACG 279
QY 41 CysGlyProCysProProArgHisTyrThrGlnPheTrrPanTyrLeuGluArgCysArg 60
Db 280 TGTGGCCCTGTTCACCGCGCCACTACACGAGTTCTGAACTACTTGAAGCGCTGGCCG 339
QY 61 TyrCysAsnValLeuCysGlyGluArgGluGluAlaArgAlaCysHisAlaThrHis 80
Db 340 TACTGCAACGTCCTCTGCGGGGAGCGTGAGAGAGGACGCGGCTTGCACGCCACCCAC 399
QY 81 AsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHis 100
Db 400 AACCGTCTCCCTGCGCGGACCGGCTTCTTCGCGCACGCTGTGTTCTGCTTGGAGCAC 459
QY 101 AlaSerCysProProGlyAlaGlyValIleAlaPro----- 112
Db 460 GCATGTGTCCACTGTCGTCGCGGCGTGAATGCCCGGGGTGAAGCTGGGCGAGGGAGGG 519
QY 112 ----- 112
Db 520 GCCCCAGAGAGTGGGCGGAGGAGTGTGGCAGGGGTCAAGTTGCTGTCGCCAGCCTTGA 579
QY 113 -----GlyThrPr 115
Db 580 CCTGAGCTAGAGACACAGTTCCTCCCTGAACCTGTTCTTCCCTCTGAGTGCAGGACCC 639
QY 115 oSerGlnAsnThrGlnCysGlnProCysProProGlyThrPheSerAlaSerSerSe 135
Db 640 CAGCCAGAACAGCGAGTCCAGCCCTGCGCCCGCCAGGACCTTCTTACGACGAGCTTCAG 699
QY 135 rSerGlnCysGlnProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValPr 155
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Db 700 CTCAGACAGTGCAGACCCCAACCGCAACTGCACGCGCCCTGGCCCTCAATGTGCC 759
QY 155 oGlySerSerSerHisAspThrLeuCysThrSerCysThrGlyPheProLeuSerThrAr 175
Db 760 AGGCTTCTTCTCCCATATACACCTTGTGACCAAGCTGACGCTTCCCTTCAGACACAG 819
QY 175 gValProGlyAlaGluGlu 181
Db 820 GGTACACAGTGACCCAGAG 838

RESULT 11
US-09-896-096A-3
; Sequence 3, Application US/09896096A
; Patent No. US20020061559A1
; GENERAL INFORMATION:
; APPLICANT: ASHKENAZI, AVI J
; APPLICANT: BOTSTEIN, DAVID
; APPLICANT: DODGE, KELLY H.
; APPLICANT: GURNEY, AUSTIN L.
; APPLICANT: KIM, KYUNG JIN
; APPLICANT: LAWRENCE, DAVID A.
; APPLICANT: PITTI, ROBERT
; APPLICANT: ROT, MARGARET A
; APPLICANT: TOMAS, DANIEL B.
; APPLICANT: WOOD, WILLIAM I.
; TITLE OF INVENTION: DCR3 Polypeptide, A TNFR Homolog
; FILE REFERENCE: P1134R2 REVISED
; CURRENT APPLICATION NUMBER: US/09/896,096A
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US 09/157,289
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: US 60/059,288
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: US 60/094,640
; PRIOR FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 18
; SEQ ID NO 3
; LENGTH: 491
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Unknown organism
; NAME/KEY: unsure
; LOCATION: 62, 73, 86, 98
; OTHER INFORMATION: unknown base
US-09-896-096A-3

Alignment Scores:
Pred. No.: 4.78e-58 Length: 491
Score: 858.00 Matches: 156
Percent Similarity: 95.71% Conservative: 0
Best Local Similarity: 95.71% Mismatches: 6
Query Match: 57.55% Indels: 1
Gaps: 0

US-09-936-024-1 (1-271) x US-09-896-096A-3 (1-491)
QY 35 ArgAspSerProThrThrCysGlyProCysProProArgHisTyrThrGlnPheTrrPan 54
Db 3 CAGACAGACCCCAACGAGTGTGGCGCCGTGTCCACCGGCGCACTACAGCGAGTTCTGGA 62
QY 55 TyrLeuGluArgCysArgTyrCysAsnValLeuCysGlyGluArgGluGluAlaArg 74
Db 63 TAACTGAGCNCCTGCGCTACTGNAACGTCTCTGNGGGAGCGCTGAAGAGGAGCGG 122
QY 75 AlaCysHisAlaThrHisAsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAla 94
Db 123 GCTTGGACACGCAACCAACCGTCTGCGCGCTGCGCGCACCGGCTTCTTGGGCAAGCT 182
QY 95 GlyPheCysLeuGluHisAlaSerCysProProGlyAlaGlyValIleAlaProGlyThr 114
Db 183 GGTTCGTGCTTGGAGCAGCATCGTGTCCACTGTGTCGCGGCGGAGATTGCCCGGGAGCC 242
|||||
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Db 181 AGCCAGAACACGAGTGCACCGCTGCCCCCAGGACCTTCTCAGCAGCAGCTCCAGC 240
Qy 136 SerGluGlnCysGlnProHisArgAsnCysThrAlaLeuLysLeuAlaLeuAsnValPro 155
Db 241 TCAGACGAGGCGCAGCCCGCAGCACTGACGCGCTGGCGCTGGCGCTGCAATGGGCCA 300
Qy 156 GlycerSerSerHisAspThrLeuCysThrSerCysThrGlyPheProLeuSerThrArg 175
Db 301 GGCTCTTCCCTCCATGACACCTCTGTGACACGCTGCACTGGCTTCCCCCTCAGACCCAG 360
Qy 176 ValProGlyAlaGluGlnCysGluArgAlaValIleAspPheValAlaPheGlnAspIle 195
Db 361 GTACCAAGAGCTGAGAGTGTGAGCGCTGCGCTCATCGACTTGTGGCTTCCAGACATC 420
Qy 196 SerIleValArgLeuGlnArgLeuLeuLeuAlaLeuGlu 208
Db 421 TCATCAAGAGGCTGACGCGCTGCTGCAAGCCCTCGAG 459

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RESULT 14 US-09-062-113-92

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Sequence 92, Application US/09062113
Patent No. US20020051969A1
GENERAL INFORMATION:
APPLICANT: GOTO, Masaki
APPLICANT: TSUDA, Eisaku
APPLICANT: MOCHIZUKI, Shin'ichi
APPLICANT: YANO, Kazuki
APPLICANT: KOBAYASHI, Fumie
APPLICANT: SHIMA, No. US20020051969A1uyuki
APPLICANT: YASUDA, Hisataka
APPLICANT: NAKAGAWA, No. US20020051969A1uaki
APPLICANT: MORINAGA, Tomonori
APPLICANT: UEDA, Masatsugu
APPLICANT: HIGASHIO, Kanji
TITLE OF INVENTION: No. US20020051969A1el Proteins and Methods for Producing
TITLE OF INVENTION: the Proteins
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
ADDRESSEE: Testa, Hurwitz & Thibault
STREET: 125 High St.
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/062,113
FILING DATE: 17-APR-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 54977/1995
FILING DATE: 20-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 207508/1995
FILING DATE: 21-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/00374
FILING DATE: 20-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,004
FILING DATE: 20-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: MOORE, Ronda P. 44,244
REGISTRATION NUMBER: 44,244
REFERENCE/DOCKET NUMBER: FCN-060DV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100

```

```

; INFORMATION FOR SEQ ID NO: 92:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 981 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..981
; OTHER INFORMATION: /note= "(OC1F-DD1)".
;
US-09-062-113-92
Alignment Scores:
Pred. No.: 2,81e-27 Length: 981
Score: 461.00 Matches: 94
Percent Similarity: 53.178 Conservative: 57
Best Local Similarity: 33.108 Mismatches: 101
Query Match: 30.924 Indels: 32
DB: Gaps: 7

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US-09-936-024-1 (1-271) x US-09-062-113-92 (1-981)

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Qy 5 ProThrTyProTPrpArgAspAlaGluThrGlyGluArgLeuValCysAlaGlnCysPro 24
Db 76 CCAAGTACCTTCATTATATGACGAAGAACTCTCATCAGCTGTGTGTGACAAATGTCCT 135
Qy 25 ProGlyThrPheValGlnArgProCysArgArgAspSerProThrCysGlyProCys 44
Db 136 CCGTGATACCTTAACCAACCACTGTACGCAAGTGAAGACCGTGCGCCCTTGC 195
Qy 45 ProProArgHisThrThrGlnPheThrPheThrPheThrLeuGluArgCysArgTrpCysAsnVal 64
Db 196 CCGTGCACCTTACTACACAGACAGCTGGACACCAAGAGAGTGTCTATCTGACGCC 255
Qy 65 LeuCysGlyGluArgGluGlnGluAlaArgAlaCysHisAlaThrHisAsnArgAlaCys 84
Db 256 GTGTGCAAGAGAGCTGACGTACGTCAAGCAGAGTGAATGACACCCCAACCGGTGTGC 315
Qy 85 ArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHisAlaSerCysPro 104
Db 316 GAATGCAAGAGAGGCGCTGCTTGAATGAGTGTGCTTGAACATGAGACCTGCGCT 375
Qy 105 ProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGlnCysGlnProCys 124
Db 376 CCGGATTTGGAGTGGTCAATGAGACCTGTAAGACACCTGTAGAAAACACACAAT 435
Qy 125 ProProGlyThrPheSerAlaSerSerSerSerSerSerGluGlnCysGlnProHisArgAsn 144
Db 436 CCAGATGGGTTCTTCTCAATGAGACCTCATCTAAGACACCTGTAGAAAACACACAAT 495
Qy 145 CysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerSerHisAspThrLeuCys 164
Db 496 TGCAGTGTCTTGTGCTCCGTCAACTCAGAAGGAATCAACACACGACCAACATA 552
Qy 165 ThrSerCysThrGlyPheProLeuSerThrArgValProGly-----AlaGluGlnCys 182
Db 553 -----TGTTCCGAAACAGTGAATCACTCAAAATGTGAATGATTGACTCTGT 606
Qy 183 GluArgAlaValIleAspPheValAlaPheGlnAspIleSerIleCysArgLeuGlnArg 202
Db 607 GAAAACAGCGTGCAGCGGCACATTGACATGCACTCACTCCTTCAGACGCTTGTGAGC 666
Qy 203 LeuLeuGlnAlaLeuGlnAlaProGluGlyTrpGlyProThrProArgAlaGlyArgAla 222
Db 667 TTGATGGAAGCTTA-----CCGGGAAGAAAGTGGAGCGAAG 705
Qy 223 AlaLeuGlnLeuLysLeuArgArg-----ArgLeuThrGluLeuLeu--- 236
Db 706 GACATTGAAAAAACATTAAGGATGCAAAACCAAGTGCACAGATCTGGAAGCTGTGACT 765
Qy 237 -----GlyAlaGlnAspGlyAlaLeuLeuValArgLeuLeuGlnAla 250

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Db 766 TTGTGGCAATAAATAATGGGACCAAGAC-----ACCTTGAAGGCGCTAATGCCAGCA 819
Qy 251 LeuArgValalaArgMetProGlyLeuGluArgSerValArgGlu----- 265
Db 820 CTAAGCACTCAAGAGCTACCACTTTCCCAAACTGTCTACTCAGAGCTCTAAAGAGACC 879
Qy 266 ---ArgPheLeu 268
Db 880 ATCAGGTTCTCT 891
RESULT 15
US-09-062-113-83
; Sequence 83, Application US/09062113
; Patent No. US20020051969A1
; GENERAL INFORMATION:
; APPLICANT: GOTO, Masaaki
; APPLICANT: TSUDA, Eisuke
; APPLICANT: MOCHIZUKI, Shin'ichi
; APPLICANT: YANO, Kazuki
; APPLICANT: KOBAYASHI, Fumie
; APPLICANT: SHIMA, No. US20020051969A1uyuki
; APPLICANT: YASUDA, Hisataka
; APPLICANT: NAKAGAWA, No. US20020051969A1uaki
; APPLICANT: MORINAGA, Tomonori
; APPLICANT: UEDA, Masatsugu
; APPLICANT: HIGASHIO, Kanji
; TITLE OF INVENTION: No. US20020051969A1el Proteins and Methods for Producing
; TITLE OF INVENTION: the Proteins
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Testa, Hurwitz & Thibault
; STREET: 125 High St.
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/062,113
; FILING DATE: 17-APR-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 54977/1995
; FILING DATE: 20-FEB-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 207508/1995
; FILING DATE: 21-JUL-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP96/00374
; FILING DATE: 20-FEB-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/915,004
; FILING DATE: 20-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: MOORE, Ronda P.
; REGISTRATION NUMBER: 44,244
; REFERENCE/DOCKET NUMBER: FJN-060DV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 83:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1206 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: -

; LOCATION: 1..1206
; OTHER INFORMATION: /note= "(OCIF-C19S)"
US-09-062-113-83
Alignment Scores:
Pred. No.: 9,39e-26 Length: 1206
Score: 442.50 Matches: 77
Percent Similarity: 57.75% Conservative: 31
Best Local Similarity: 41.18% Mismatches: 74
Query Match: 29,68% Indels: 5
DB: 10 Gaps: 2
US-09-936-024-1 (1-271) x US-09-062-113-83 (1-1206)
Qy 5 ProThrTyrProTyrArgAspAlaGluThrGlyGluArgLeuValCysAlaGlnCysPro 24
Db 76 CCNAAGTACTTCATTATGACGAGAAACCTCTCATCAGCTGTGTGTGACAAATGTCT 135
Qy 25 ProGlyThrPheValGlnArgProCysArgAspSerProThrThrCysGlyProCys 44
Db 136 CCTGGTACTACCTAAACAAACACTGTACAGCAAAAGTGGAGACCGGTGTGGCCCTTGC 195
Qy 45 ProProArgHisTyrThrGlnPheTyrAsnTyrLeuGluArgCysArgTyrCysAsnVal 64
Db 196 CCTGACCCTACTACACAGACAGCTGGCACACCCAGTGCAGAGTGTCTATCTGCAGCCCC 255
Qy 65 LeuCysGlyGluArgGluGluAlaArgAlaCysHisAlaThrHisAsnArgAlaCys 84
Db 256 GTGTGCAAGGAGCTGCAGTACGTCAAGCAGGAGTGCATTCGCCACCACCCCGGTGTGC 315
Qy 85 ArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHisAlaSerCysPro 104
Db 316 GAATGCAAGGAAGGCGCTACCTTGAGATAGAGTTCCTGTTGAAACATAGGAGTGCCT 375
Qy 105 ProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGlnCysGlnProCys 124
Db 376 CCTGGATTGGAGTGTGTGCAAGCTGGAAACCCAGAGCGAATAACAGTTTGCAAAAGATGT 435
Qy 125 ProProGlyThrPheSerAlaSerSerSerSerGluGlnCysGlnProHisArgAsn 144
Db 436 CCAGATGGGTTCTTCTCAATGAGAGCTCATCTAAGCACCCTGTAGAAAACACACAAAT 495
Qy 145 CysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerSerHisAspThrLeuCys 164
Db 496 TGCAGTGTCTTTGGTCTCTCTGCTAACTCAGAAAGGAATGCAACACACACACACATA--- 552
Qy 165 ThrSerCysThrGlyPheProLeuSerThrArgValProGlyAlaGluGlu-----Cys 182
Db 553 -----TGTTCGGAACACAGTGAATCACTCAAAAAAGTGAATAGATGTACCCCTGTGT 606
Qy 183 GluArgAlaValIleAspPhe 189
Db 607 GAGGAGGCATTCTTCAGGTTT 627
Search completed: January 6, 2003, 13:48:04
Job time : 136 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 6, 2003, 12:54:06 / Search time 2673 Seconds

(without alignments)
8851.695 Million cell updates/sec

Title: US-09-936-024-2

Perfect score: 813

Sequence: 1 gtggcagaacaccaccta.....agccttcctcctcgtgcac 813

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapept 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

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2: gb_hcg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
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38: em_sy:*
39: em_hlgo_hum:*
40: em_hlgo_mus:*
41: em_hlgo_other:*
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	813	100.0	813	6 AX119833	AX119833 Sequence
2	813	100.0	813	6 AX167223	AX167223 Sequence
3	813	100.0	813	6 AX375169	AX375169 Sequence
4	813	100.0	903	9 AF134240	AF134240 Homo sapi
5	813	100.0	1048	9 AF217794	AF217794 Homo sapi
6	813	100.0	1055	6 AX082868	AX082868 Sequence
7	813	100.0	1114	6 AX055373	AX055373 Sequence
8	813	100.0	1114	6 AX056645	AX056645 Sequence
9	813	100.0	1114	9 AF104419	AF104419 Homo sapi
10	813	100.0	1125	9 BC017065	BC017065 Homo sapi
11	813	100.0	1168	6 AX017828	AX017828 Sequence
12	813	100.0	1347	6 AR171895	AR171895 Sequence
13	813	100.0	1428	9 AF217793	AF217793 Homo sapi
14	813	100.0	4945	9 AB029011	AB029011 Homo sapi
15	811.4	99.8	1150	9 BC034349	BC034349 Homo sapi
16	811.4	99.8	5769	9 HSM802484	AL157435 Homo sapi
17	809.8	99.6	936	6 AX093178	AX093178 Sequence
18	809.8	99.6	936	6 AX097545	AX097545 Sequence
19	809.8	99.6	936	6 AX098029	AX098029 Sequence
20	809.8	99.6	936	6 AX119836	AX119836 Sequence
21	809.8	99.6	936	6 AX167230	AX167230 Sequence
22	809.8	99.6	936	6 AX375171	AX375171 Sequence
23	533.4	65.6	1859	6 AR171896	AR171896 Sequence
24	459	56.5	459	6 AR171887	AR171887 Sequence
25	385.8	47.5	120917	9 HSJ583P15	AL121845 Human DNA
26	381	46.9	114793	9 AF217796	AF217796 Homo sapi
27	216.8	26.7	925	6 AX251528	AX251528 Sequence
28	216.8	26.7	925	6 AX346745	AX346745 Sequence
29	190.8	23.5	925	6 AX251527	AX251527 Sequence
30	190.8	23.5	925	6 AX346744	AX346744 Sequence
31	129.6	15.9	525	6 AR099131	AR099131 Sequence
32	121	14.9	1116	5 AF401631	AF401631 Oncorhinc
33	117.8	14.5	1148	5 OMV315137	AJ315137 Oncorhinc
34	112	13.8	2432	6 AR168728	AR168728 Sequence
35	112	13.8	2432	6 AR205587	AR205587 Sequence
36	112	13.8	2432	6 AX076604	AX076604 Sequence
37	112	13.8	2432	10 RNU94330	U94330 Rattus norv
38	110.4	13.6	1324	6 AR168729	AR168729 Sequence
39	110.4	13.6	1324	6 AR205588	AR205588 Sequence
40	110.4	13.6	1325	10 MMU94331	U94331 Mus muscu
41	108.8	13.4	2818	10 AB013898	AB013898 Mus muscu
42	107.2	13.2	1325	6 AX076606	AX076606 Sequence
43	103	12.7	1166	9 AF134187	AF134187 Homo sapi
44	103	12.7	1206	6 E15271	E15271 Human mRNA
45	103	12.7	1206	9 AB002146	AB002146 Homo sapi

ALIGNMENTS

RESULT 1	LOCUS	AX119833	813 bp	DNA	linear	PAT 11-MAY-2001
DEFINITION	Sequence 2 from Patent WO0128582.					
ACCESSION	AX119833					
VERSION	AX119833.1	GI:14036593				
KEYWORDS						
SOURCE	human.					
ORGANISM	Homo sapiens					
REFERENCE	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.					
TITLE	Bumol, T.F. and Cohen, P.J.					
JOURNAL	Therapeutic applications of flint polypeptides					
	Patent: WO 0128582-A 2 26-APR-2001;					

Db	721	GGGCGGCTGCTGTGTGCAGTGTGTGCAGAGCGCTGCCCGTCAGACAGATGCCCCGGCTGGAG	780
OY	781	CGAGCGTCCGTGAGCGCTTCTCCTCCTGTGCAC	813
Db	781	CGAGCGTCCGTGAGCGCTTCTCCTCCTGTGCAC	813
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LOCUS	AXJ375169	813 bp	DNA
DEFINITION	Sequence 2 from Patent WO0209668.		linear
ACCESSION	AXJ375169		PAT 01-MAR-2002
VERSION	AXJ375169.1	GI:19169920	
KEYWORDS			
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Micanovic,R. and Wlitcher,D.R.		
TITLE	Pulmonary administration of flint		
JOURNAL	Patent: WO 0209668-A 2 07-FEB-2002;		
FEATURES	ELI LILLY AND COMPANY (US)		
source	Location/Qualifiers		
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	/db_xref="taxon:9606"		
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Best Local Similarity	100.0%; Pred. No. 7e-125;		
Matches 813; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
OY	1	GNGCGAAGAAACACCACCTAACCCCTGGGGGAGCGAGAACAAGGGGAGCGGCTGTGTC	60
Db	1	GTGGCAAGAAACACCACCTAACCCCTGGGGGAGCGAGAACAAGGGGAGCGGCTGTGTC	60
OY	61	GCCCATGCCCCCCCAGGACACTTTTGAGAGCGGGCGTGCCTGCAGACAGCCCCAGAG	120
Db	61	GCCCATGCCCCCCCAGGACACTTTTGAGAGCGGGCGTGCCTGCAGACAGCCCCAGAG	120
OY	121	TGTGGCCCCGTGTCACCGGCGCACCTACACAGCATTTCTGGAACTACCTGAGAGCGTCCGC	180
Db	121	TGTGGCCCCGTGTCACCGGCGCACCTACACAGCATTTCTGGAACTACCTGAGAGCGTCCGC	180
OY	181	TACTGCAACGTCCTTTGGGGGAGAGGTGAGAGGAGCAAGGGCTTGCACGCCACCCAC	240
Db	181	TACTGCAACGTCCTTTGGGGGAGAGGTGAGAGGAGCAAGGGCTTGCACGCCACCCAC	240
OY	241	AACCGTGCCTGGCGGTGCGCGACCGGCTTCTTGGCGACGCTGGTTCTTGCTTGAGGAC	300
Db	241	AACCGTGCCTGGCGGTGCGCGACCGGCTTCTTGGCGACGCTGGTTCTTGCTTGAGGAC	300
OY	301	GCATGTGTCACCTGTGTGCGGCGTGAATTGCCCGGGACCCCCAGCAGAACAGGAG	360
Db	301	GCATGTGTCACCTGTGTGCGGCGTGAATTGCCCGGGACCCCCAGCAGAACAGGAG	360
OY	361	TGCCAGCGGTGCCCCCGGACCACTTCTCAGCCAGCAGTCCAAGCTCAGAGCAGTGGCAG	420
Db	361	TGCCAGCGGTGCCCCCGGACCACTTCTCAGCCAGCAGTCCAAGCTCAGAGCAGTGGCAG	420
OY	421	CCCCACCGCAACTGACAGGGCCCTGGGGCCCTGAGCCCTCAATGTGCCAGAGGCTCTTCCCTCAT	480
Db	421	CCCCACCGCAACTGACAGGGCCCTGGGGCCCTGAGCCCTCAATGTGCCAGAGGCTCTTCCCTCAT	480
OY	481	GACACCTGTGTGACCAAGCTGCACTGGCTTCCCCCTCAGACACCAAGGATAACAGAGCTGAG	540
Db	481	GACACCTGTGTGACCAAGCTGCACTGGCTTCCCCCTCAGACACCAAGGATAACAGAGCTGAG	540
OY	541	GAGTGTGACGCTGCGCTGATGCACTTTGTGGCTTTTCAGAGACATTCATCAAGAAGGCTG	600
Db	541	GAGTGTGACGCTGCGCTGATGCACTTTGTGGCTTTTCAGAGACATTCATCAAGAAGGCTG	600

Oy	601	CAGGCGCTGTCGACAGGGCCCTTGAGGCCCCCAGGAGGGCTTGGGTCCGACACCAAGGCGGGC	660
Dd	601	CAGCGGCTGTCGACAGGCCCTTGAGGCCCCCAGGAGGGCTTGGGTCCGACACCAAGGCGGGC	660
Oy	661	CGCGCGGCTTGCAGACTGACCTGGTCGGCGGGCTCACGGAAGCTCTGGGGCCGAGAAC	720
Dd	661	CGCGCGGCTTGCAGACTGACCTGGTCGGCGGGCTCACGGAAGCTCTGGGGCCGAGAAC	720
Oy	721	GGGGCGCTGTCGTGTGGCGGCTGCTGTCAGAGCGCTGGCGCGTGGCCAGATGCCCGGGCTGAG	780
Dd	721	GGGGCGCTGTCGTGTGGCGGCTGCTGTCAGAGCGCTGGCGCGTGGCCAGATGCCCGGGCTGAG	780
Oy	781	CGGAGCGTCGTTGAGCGGCTTCTCCCTGTGTGAC	813
Dd	781	CGGAGCGTCGTTGAGCGGCTTCTCCCTGTGTGAC	813

RESULT 4	AFI34240	903 bp	mRNA	linear	PRI 11-MAY-1999
LOCUS	AFI34240				
DEFINITION	Homo sapiens tumor necrosis factor receptor homolog (TR6) mRNA,				
ACCESSION	AFI34240				
VERSION	AFI34240.1	GI:4768938			
KEYWORDS					
SOURCE	Homo sapiens.				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.				
REFERENCE	1. (bases 1 to 903)				
AUTHORS	Yu, K.Y., Kwon, B., Ni, J., Zhai, Y., Ebner, R. and Kwon, B.S.				
TITLE	A newly identified member of tumor necrosis factor receptor				
JOURNAL	superfamily (TR6) suppresses LIGHT-mediated apoptosis				
MEDLINE	J. Biol. Chem. 274 (20), 13733-13736 (1999)				
PUBMED	99253915				
10318773					
REFERENCE	2. (bases 1 to 903)				
AUTHORS	Kwon, B.S. and Yu, K.Y.				
TITLE	Direct Submission				
JOURNAL	Submitted (10-MAR-1999) Micro/Immuno1, Indiana University, 635				
	Barnhill Drive, Indianapolis, IN 46202, USA				
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gene	1..903-				
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CDS	1..903				
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	ERLVCAQCPGTFVQRCDRSDSPTCGPCEPRHYTOPWNLERYCNVLCGEREEBA				
	RACHATNRAKRCRTGFFAHAGCLEHASCPGAGVIAPGPSNTGOCPCPGTFSA				
	SSSESCOPCHRNCTALGLANVGSSSHDTLCSCTGPLSTVPAGEEERAVIDFE				
	VARDISIKRLRIQLTLLEAPEGMGPPRRGRBALQKLKRRLTELLGAQDGLLVLL				
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BASE COUNT	129 a	324 c	305 g	145 t
ORIGIN				
Query Match	100.0%;	Score 813;	DB 9;	Length 903;
Best Local Similarity	100.0%;	Pred. No. 6, 8e-125;		
Matches 813;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Oy	1	GTGGCAGAAACACCACCTACCCCTTGCGGGAGCGCAGACAGAGGGAGCGGCTGGTGTC	60
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Db 148 GCCAGTGCCTCCAGGACCTTTGTGAGCGCGCTGCGCCGAGACAGCCCCACGACG 207
QY 121 TGTGGCCGCTGTCACCGCGCCACTACACGAGTTCTGGAATCTACCTGGAGCGCTGCCGC 180
Db 208 TGTGGCCGCTGTCACCGCGCCACTACACGAGTTCTGGAATCTACCTGGAGCGCTGCCGC 267
QY 181 TACTGCAACGCTCTCTGCGGGAGCGTGTAGAGAGGACGCGGTTCGCACGCCACCCAC 240
Db 268 TACTGCAACGCTCTCTGCGGGAGCGTGTAGAGAGGACGCGGTTCGCACGCCACCCAC 327
QY 241 AACCGTGCCTGCCCTGCCGACCGCTTCTTCCGCAACGCTGTTCTGTTGGAGCAC 300
Db 328 AACCGTGCCTGCCCTGCCGACCGCTTCTTCCGCAACGCTGTTCTGTTGGAGCAC 387
QY 301 GCATCTGTCTCACCTGTGCGCGCGTGAATGCGCCCGGCGCACCCCGACCAACACGACG 360
Db 388 GCATCTGTCTCACCTGTGCGCGCGTGAATGCGCCCGGCGCACCCCGACCAACACGACG 447
QY 361 TGCCAGCGGTGCCCTCCAGGACCTTCTCAGCCAGAGCTCCAGCTCAGAGCAGTGCCAG 420
Db 448 TGCCAGCGGTGCCCTCCAGGACCTTCTCAGCCAGAGCTCCAGCTCAGAGCAGTGCCAG 507
QY 421 CCCACCGCACTGCAGCGCCCTGGCGCTTCCGCTCAATGTCAGGCTCTTCTCTCCCAT 480
Db 508 CCCACCGCACTGCAGCGCCCTGGCGCTTCCGCTCAATGTCAGGCTCTTCTCTCCCAT 567
QY 481 GACACCTGTGCACAGCTGCACCTGCTTCCCTCAGCACCAGGCTACCAAGAGCTGAG 540
Db 568 GACACCTGTGCACAGCTGCACCTGCTTCCCTCAGCACCAGGCTACCAAGAGCTGAG 627
QY 541 GAGTGTGAGCGTGCCGTCATGACTTTGTGGCTTTTCAGGACATCTCCATCAAGAGCTG 600
Db 628 GAGTGTGAGCGTGCCGTCATGACTTTGTGGCTTTTCAGGACATCTCCATCAAGAGCTG 687
QY 601 CAGCGCTGTGTCAGCGCTTGCAGCGCCCGGAGGCTGGGGTCCGACACCAAGGGCGGGC 660
Db 688 CAGCGCTGTGTCAGCGCTTGCAGCGCCCGGAGGCTGGGGTCCGACACCAAGGGCGGGC 747
QY 661 CGCGCGCTTTCAGCTGAAAGCTCGCTCGCGGCTCAGCGAGCTCTCGGGGGCGCAGGAC 720
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QY 721 GGGCGCTGTGCTGCGCTGCTCAGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGAG 780
Db 808 GGGCGCTGTGCTGCGCTGCTCAGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGAG 867
QY 781 CGGAGCTCCGTGAGCGCTTCTCTCCCTGTGCAC 813
Db 868 CGGAGCTCCGTGAGCGCTTCTCTCCCTGTGCAC 900

RESULT 5
AF217794 AF217794 1048 bp mRNA linear PRI 12-FEB-2000
LOCUS Homo sapiens M68E mRNA, alternatively spliced, complete cds.
DEFINITION AF217794
ACCESSION AF217794
VERSION AF217794.1 GI:696262
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1048)
AUTHORS Bai, C., Connolly, B., Metzker, M.L., Hilliard, C.A., Liu, X., Sandig, V., Soderman, A., Galloway, S.M., Liu, Q., Austin, C.P. and Caskey, C.T.
TITLE Overexpression of M68/Dcr3 in human gastrointestinal tract tumors independent of gene amplification and its location in a four-gene cluster
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (3), 1230-1235 (2000)

MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source

20122600
10655513
2 (bases 1 to 1048)
Bai, C.
Direct Submission
Submitted (21-DEC-1999) WP26A-1000, Merck Research Laboratories,
Summeytown Pike, West Point, PA 19403, USA
Location/Qualifiers
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/db_xref="taxon:9606"
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SSSSSEOCOPHENCTALGLALNVPGSSSHDTLCTCTGTPPLSTRVPGARECAVIDF
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CDS

BASE COUNT 160 a 367 c 335 g 186 t
ORIGIN
Query Match 100.0%; Score 813; DB 9; Length 1048;
Best Local Similarity 100.0%; Pred. No. 6.6e-125; Mismatches 0; Indels 0; Gaps 0;
Matches 813; Conservative 0;

QY 1 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGACAGACAGGGGAGCGGCTGGTGTC 60
Db 140 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGACAGACAGGGGAGCGGCTGGTGTC 199
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QY 121 TGTGGCCGCTGTCACCGCGCCACTACACGAGTTCTGGAATCTACCTGGAGCGCTGCCGC 180
Db 260 TGTGGCCGCTGTCACCGCGCCACTACACGAGTTCTGGAATCTACCTGGAGCGCTGCCGC 319
QY 181 TACTGCAACGCTCTCTGCGGGAGCGTGTAGAGAGGACGCGGTTCGCCACGCCACCCAC 240
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QY 241 AACCGTGCCTGCCCTGCCGACCGCTTCTTCCGCAACGCTGTTCTGTTGGAGCAC 300
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QY 301 GCATCTGTCTCACCTGTGCGCGCGTGAATGCGCCCGGCGCACCCCGACCAACACGACG 360
Db 440 GCATCTGTCTCACCTGTGCGCGCGTGAATGCGCCCGGCGCACCCCGACCAACACGACG 499
QY 361 TGCCAGCGGTGCCCTCCAGGACCTTCTCAGCCAGAGCTCCAGCTCAGAGCAGTGCCAG 420
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QY 421 CCCACCGCAACTGCACCGCGCTTGGCGCTTCCGCTCAATGTCAGGCTCTTCTCTCCCAT 480
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Db 620 GACACCTGTGCACAGCTGCACCTGCTTCCGCTCAGCACCAGGCTACCAAGAGCTGAG 679
QY 541 GAGTGTGAGCGTGCCGTCATGACTTTGTGGCTTTTCAGGACATCTCCATCAAGAGGCTG 600
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QY 661 CCGCGCGCTTCGACGCTGGAAGCTGCTGGCGGCTTCACCGAGCTCTGGGGGCGCAGAC 720
DB 800 CCGCGCGCTTCGACGCTGGAAGCTGCTGGCGGCTTCACCGAGCTCTGGGGGCGCAGAC 859
QY 721 GGGGCGCTGCTGGGCGGCGCTGTCAGGCGCTGGCGGCGCAGAGTCCCGGCGCTGAG 780
DB 860 GGGGCGCTGCTGGGCGGCGCTGTCAGGCGCTGGCGGCGCAGAGTCCCGGCGCTGAG 919
QY 781 CCGAGCGCTCCGTGAGCGCTTCCTCTCTGTCAC 813
DB 920 CGAGCGCTCCGTGAGCGCTTCCTCTCTGTCAC 952

RESULT 6
AX082868 1055 bp DNA linear PAT 28-FEB-2001
LOCUS Sequence 1 from Patent WO0110908.
ACCESSION AX082868
VERSION AX082868.1 GI:13184802
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Hsu, H.
TITLE Ntr3, a member of the tnf-receptor supergene family
JOURNAL Patent: WO 0110908-A 1 15-FEB-2001;
Amgen Inc. (US)

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source location/Qualifiers
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CDS
160 a 369 c 340 g 186 t

BASE COUNT 160 a 369 c 340 g 186 t
ORIGIN

Query Match 100.0%; Score 813; DB 6; Length 1055;
Best Local Similarity 100.0%; Pred. No. 6, 6e-125;
Matches 813; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGCAGAAACACCACTACCTCTGGCGGACGACAGAGAGAGGAGCGGCTGTGTC 60
DB 154 GTGGCAGAAACACCACTACCTCTGGCGGACGACAGAGAGAGGAGCGGCTGTGTC 213
QY 61 GCCCAGTGCCTCCGAGGACCTTTGTGACGCGCGCTGCGCCGAGACAGCGCCACGACG 120
DB 214 GCCCAGTGCCTCCGAGGACCTTTGTGACGCGCGCTGCGCCGAGACAGCGCCACGACG 273
QY 121 TGTGGCCCTGTGTCACCGCGCACTACACGAGTTTGGAACTACTTGGAGCGCTGCGCG 180
DB 274 TGTGGCCCTGTGTCACCGCGCACTACACGAGTTTGGAACTACTTGGAGCGCTGCGCG 333
QY 181 TACTGCAACGCTCTCTGCGGGAGCGTGAAGAGAGGACGCGCTTGCACGCCACCCAC 240
DB 334 TACTGCAACGCTCTCTGCGGGAGCGTGAAGAGAGGACGCGCTTGCACGCCACCCAC 393
QY 241 AACGTGCTGCGCTGCGGACCGGCTTTCTTCCGACACGCTGTGTTCTGTGAGACAC 300

DB 394 AACGTGCTGCGCTGCGGACCGGCTTCTTCCGACACCTGTGTTCTGTGAGAC 453
QY 301 GCATCGTGCACCTGCTGTCGCGGCTGATGATGCGCGGACCGCCAGCCAGACAGCAG 360
DB 454 GCATCGTGCACCTGCTGTCGCGGCTGATGATGCGCGGACCGCCAGCCAGACAGCAG 513
QY 361 TGCAGCGCTGCGCGCGGACGACCTTCTCAGCAGCAGCTTCAGCTCAGAGAGTGCAG 420
DB 514 TGCAGCGCTGCGCGCGGACGACCTTCTCAGCAGCAGCTTCAGCTCAGAGAGTGCAG 573
QY 421 CCCACCGCACTGACAGCGGCTTGGGCTTGGCCCTCAATGTGCGAGGCTTCTTCCAT 480
DB 574 CCCACCGCACTGACAGCGGCTTGGGCTTGGCCCTCAATGTGCGAGGCTTCTTCCAT 633
QY 481 GACACCTGTGACACGAGCTGACCTTGTCCCTCAGACACGAGGTACAGAGAGCTGAG 540
DB 634 GACACCTGTGACACGAGCTGACCTTGTCCCTCAGACACGAGGTACAGAGAGCTGAG 693
QY 541 GAGTGTAGCGGTGCGCGCTGATCGACTTGTGGCTTTCAGAGACATCTTCATCAAGGCTG 600
DB 694 GAGTGTAGCGGTGCGCGCTGATCGACTTGTGGCTTTCAGAGACATCTTCATCAAGGCTG 753
QY 601 CAGGCGCTGCTGACAGGCGCTTCAGAGCCCGAGGCGCTGGGCTCCGACCAAGGCGGCG 660
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DB 814 CCGCGCGCTTCGACGCTGGAAGCTGCTGCGCGCTTCACGAGCTCTGGGGGCGCAGAC 873
QY 721 GGGGCGCTGCTGGGCGGCGCTGTCAGGCGCTGGCGGCGCTGGCCAGAGATCCCGGCGTGGAG 780
DB 874 GGGGCGCTGCTGGGCGGCGCTGTCAGGCGCTGGCGGCGCTGGCCAGAGATCCCGGCGTGGAG 933
QY 781 CCGAGCGCTCCGTGAGCGCTTCCTCTCTGTCAC 813
DB 934 CGAGCGCTCCGTGAGCGCTTCCTCTCTGTCAC 966

RESULT 7
AX055373 1114 bp DNA linear PAT 13-JAN-2001
LOCUS Sequence 3 from Patent WO0073452.
ACCESSION AX055373
VERSION AX055373.1 GI:12228659
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Ashkenazi, A.J., Baker, K.P., Chan, B., Goddard, A., Godowski, P.J.,
Gurney, A.L., Hebert, C., Henzel, W., Kabakoff, R.C., Shelton, D.L.,
Tumas, D., Watanabe, C.K. and Wood, W.I.
TITLE Compositions and methods for the treatment of immune related
diseases
JOURNAL Patent: WO 0073452-A 3 07-DEC-2000;
Genentech, Inc. (US)

FEATURES
source location/Qualifiers
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/db_xref="taxon:9606"
188 a 379 c 356 g 191 t

BASE COUNT 188 a 379 c 356 g 191 t
ORIGIN

Query Match 100.0%; Score 813; DB 6; Length 1114;
Best Local Similarity 100.0%; Pred. No. 6, 6e-125;
Matches 813; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGCAGAAACACCACTACCTCTGGCGGACGACAGAGAGAGGAGCGGCTGTGTC 60
DB 188 GTGGCAGAAACACCACTACCTCTGGCGGACGACAGAGAGAGGAGCGGCTGTGTC 247

Source	Organism	Title	Journal	Medline	PubMed	Reference	Authors	Gene	CDS
Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	1 (bases 1 to 1114)					Pitli, R.M., Marsters, S.A., Lawrence, D.A., Roy, M., Kischkel, F.C., Dowd, P., Huang, A., Donahue, C.J., Sherwood, S.W., Baldwin, D.T., Godowski, P.J., Wood, W.I., Gurney, A.L., Hillan, K.J., Cohen, R.L., Goddard, A.D., Botstein, D. and Ashkenazi, A.	Direct Submission	
		Submitted (04-NOV-1998)	Molecular Oncology, Genentech, 1 DNA Way, San Francisco, CA 94080, USA						
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		248 GCCCAGTCCCCCGACGACCTTTGTGACAGCGCGCGTGCCTCGAGACACCCCGACGAC							
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		241 AACCGTCCCTGCGGACCGGACGAGCTTTCTTGCAGCAGCTGCTTTCTGCTTGAAC							

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D	b	488	GCATGTGTCCACTCTGTGTGCCGGCGTGAATTGCCGCCACCACCAGCAACGCGAG	547
O	y	361	TGCCAGCCGTCCCCCCCAGGACCTTCTCCACCCAGACACTCCAGTCAAGACATGCCAG	420
D	b	548	TGCCAGCCGTCCCCCCCAGGACCTTCTCCACCCAGACACTCCAGTCAAGACATGCCAG	607
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D	b	668	GACACCCCTGTSCACACGAGCTGACATTGGCTTCCCTCAGACACCAAGGTAACAAGACTGAG	727
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D	b	788	CAGCGGCTGTGACAGAGCCCTGAGAGCCCGGAGAGGCTGGGGTCCGACACAAAGGCGGGC	847
O	y	661	CGCGGGGCTTGTGACAGCTGMACTGGCTGGGCGGCTCAAGAGCTTCTGGGGCGCAGAGAC	720
D	b	848	CGCGGGGCTTGTGACAGCTGMACTGGCTGGGCGGCTCAAGAGCTTCTGGGGCGCAGAGAC	907
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RESULT 10 .
LOCUS BC017065
DEFINITION Homo sapiens, tumor necrosis factor receptor superfamily, member 6d, decoy, clone MGC:9587 IMAGE:3886635, mRNA, complete cds.
ACCESSION BC017065
VERSION MGC17065.1 GI:16877637
KEYWORDS MGC.
SOURCE Homo sapiens.
ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1125)
AUTHORS Strausberg,R.
TITLE Direct Submission
JOURNAL Submitted (05-NOV-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: MGC help desk
Email: cgaps-i@mail.nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found

through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAK Plate: 22 Row: d Column: 23
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 14790166.

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BASE COUNT      200 a 378 c 356 g 191 t
ORIGIN
Query Match      100.0%; Score 813; DB 9; Length 1125;
Best Local Similarity 100.0%; Pred. No. 6.5e-125;
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Db 187 GTGGCAGAAACACCCACTTACCCCTGCGGGACGACAGAGGAGCGGCTGGTGTGC 246
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ACCESSION      AX017828
VERSION      AX017828.1      GI:10042431
KEYWORDS
SOURCE      human.
ORGANISM      Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 1168)
AUTHORS      Kroeger, B.
TITILE      Receptor, from the superfamily of tnt-receptors from the human lung
JOURNAL      Patent: WO 9946376-A 1 16-SEP-1999;
BASF AG (DE); KROEGER BURKHARD (DE)
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DEFINITION Sequence 18 from patent US 6297367.
ACCESSION AR171895
VERSION AR171895.1 GI:17910845
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 1347)
AUTHORS Triboley, C.
TITLE Polynucleotide encoding TNF1
JOURNAL Patent: US 6297367-A 18 02-OCT-2001;
FEATURES
source 1.1347
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ORIGIN

Query Match 100.0%; Score 813; DB 6; Length 1347;
Best Local Similarity 100.0%; Pred. No. 6.3e-125;
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RESULT 13
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DEFINITION Homo sapiens M68C mRNA, alternatively spliced, complete cds.
ACCESSION AF217793
VERSION AF217793.1 GI:6969260
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
REFERENCE 1 (bases 1 to 1428)
AUTHORS Bal, C., Connolly, B., Metzger, M.L., Hilliard, C.A., Liu, X., Sandig, V., Soderman, A., Galloway, S.M., Liu, Q., Austin, C.P. and Caskey, C.T.
TITLE Overexpression of M68/DCR3 in human gastrointestinal tract tumors independent of gene amplification and its location in a four-gene cluster
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (3), 1230-1235 (2000)
MEDLINE 20122600
PUBMED 10655513
REFERENCE 2 (bases 1 to 1428)
AUTHORS Bal, C.
TITLE Direct Submission
JOURNAL Submitted (21-DEC-1999) WP26A-1000, Merck Research Laboratories,

	Sunneytown Pike, West Point, PA 19403, USA	
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Db	882	TGCCAGCGGTGCCCCCAGGACCTTCTCAGCGACAGCTCCAGCTCAGACGATGCCAG	941	
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ORCOAWORHLOASBMCSPACHTASRKOSVQWVPPPHDHBGABRVAAPVGVGA
ACPAAGAGCTSRNTHPLAGHRKAGVREVPFRHLCAAVPPROPHDWPVSTA
PLHAVLELGPALPLQRPURGA"

BASE COUNT 963 a 1581 c 1529 g 872 t
ORIGIN

Query Match 100.0%; Score 813; DB 9; Length 4945;

Best Local Similarity 100.0%; Pred. No. 4.9e-125;

Matches 813; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GTGACAGAAACACCACTACCCCTGGCGGAGACAGAGAGAGCGGCTGTGTGC 60

DB 3995 GTGACAGAAACACCACTACCCCTGGCGGAGACAGAGAGAGCGGCTGTGTGC 4054

QY 61 GCCCAGTGCCTCCCGAGGACCTTTGTGACGCGCCGCGCGAGACAGCCCGACG 120

DB 4055 GCCCAGTGCCTCCCGAGGACCTTTGTGACGCGCCGCGCGAGACAGCCCGACG 4114

QY 121 TGTGGCCCGTGTACACCGCCCACTACAGCAGTTCTGGAATCTCTGAGCGCTGCCG 180

DB 4115 TGTGGCCCGTGTACACCGCCCACTACAGCAGTTCTGGAATCTCTGAGCGCTGCCG 4174

QY 181 TACTGCAACGCTCTGTGCGGGAGCGTAGAGAGAGGACGCGCTTGCCAGCGCAC 240

DB 4175 TACTGCAACGCTCTGTGCGGGAGCGTAGAGAGAGGACGCGCTTGCCAGCGCAC 4224

QY 241 AACCGTCCGTGCGCTCCCGACCGGCTTTCTGCGCAGCGTGTGTTCTGCTTGAAC 300

DB 4235 AACCGTCCGTGCGCTCCCGACCGGCTTTCTGCGCAGCGTGTGTTCTGCTTGAAC 4294

QY 301 GCATCGTGTCACTGTGTGCGGGATGATGATGATGATGATGATGATGATGATGATG 360

DB 4295 GCATCGTGTCACTGTGTGCGGGATGATGATGATGATGATGATGATGATGATGATG 4354

QY 361 TGGCAGCGTGCCTCCCGAGGACCTTTCTGCGCAGCGTGTGTTCTGCTTGAAC 420

DB 4355 TGGCAGCGTGCCTCCCGAGGACCTTTCTGCGCAGCGTGTGTTCTGCTTGAAC 4414

QY 421 CCCACCGCACTGCAAGGCGCTGCGCTGCGCTCAATGTGCGAGGCTTCTCCCAT 480

DB 4415 CCCACCGCACTGCAAGGCGCTGCGCTGCGCTCAATGTGCGAGGCTTCTCCCAT 4474

QY 481 GACAACCTGTGCACTGCAAGGCGCTGCGCTGCGCTCAATGTGCGAGGCTTCTCCCAT 540

DB 4475 GACAACCTGTGCACTGCAAGGCGCTGCGCTGCGCTCAATGTGCGAGGCTTCTCCCAT 4534

QY 541 GAGGTAGAGGTGCGCTGCACTGCTTGTGCTTCAAGGACATCTCATTAAGAGCTG 600

DB 4535 GAGGTAGAGGTGCGCTGCACTGCTTGTGCTTCAAGGACATCTCATTAAGAGCTG 4594

QY 601 CAGCGCTGTGCAAGGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTG 660

DB 4595 CAGCGCTGTGCAAGGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTG 4654

QY 661 CCGCGCGCTTGTGCACTGCAAGGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCG 720

DB 4655 CCGCGCGCTTGTGCACTGCAAGGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCG 4714

QY 721 GGGGCGCTGTGCGCTGCTGCAAGGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCG 780

DB 4715 GGGGCGCTGTGCGCTGCTGCAAGGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCG 4774

QY 781 CGGAGCGTCCGTGAGCGCTTCTCTCTGTGCA 813

DB 4775 CGGAGCGTCCGTGAGCGCTTCTCTCTGTGCA 4807

RESULT 15

BC034349

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

REMARK

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NOTE

BC034349 1150 bp mRNA linear PRI 08-JUL-2002
Homo sapiens, tumor necrosis factor receptor superfamily, member
6b, decoy, clone MGC:21079 IMAGE:4752507, mRNA, complete cds.
BC034349
BC034349.1 GI:21706464
MGC.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 1150)
Strausberg, R.
Direct Submission
Submitted (02-JUL-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: <http://mgc.ncl.nih.gov>
Contact: MGC help desk
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: James Cleaver, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
Contact: amg@bcm.tmc.edu
Gunnar, P.H., Garcia, A.M., Lu, X., Hilyk, S.W., Hale, S.M.,
Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M.,
Richards, S., Gibbs, R.A.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>
Series: IRK Plate: 28 Row: 0 Column: 15
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 14790166.
Location/Qualifiers
1. 1150
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="MGC:21079 IMAGE:4752507"
/issue_type="Skin, squamous cell carcinoma"
/clone_lib="NCI CGAP_Skn4"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6.ccdB"
109..1011
/codon_start=1
/product="tumor necrosis factor receptor superfamily,
member 6b, decoy"
/protein_id="AAH34349.1"
/db_xref="GI:21706465"
/db_xref="LocusID:8771"
/translation="KMALEGGSLICLVALLPALLPVAAGVATPTPYPRDAETG
ERLVACQCPPTGTVRPPCRDPTTCGPPRHYTOFMYVLRRCRYNLCGERBEA
RACHATNACRCRTGFPAHAGSCFENHACSPGAGVIAIGTSPONTQCPGPTSA
SSSSBOCQPHNCTALGALNVPGSSHDITCTSGTGPLSTRVGAECERAVIDF
VAFODISRIQRLQALAPRGMGPTPAGAAALQKLRRLTILGADGALLVRL
LQALRYARMPGLERSVREFFLVH"

BASE COUNT 222 a 382 c 348 g 198 t
ORIGIN

Query Match 99.8%; Score 811.4; DB 9; Length 1150;

Best Local Similarity 99.8%; Pred. No. 1.2e-124;

Matches 812; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 GTGACAGAAACACCACTACCCCTGGCGGAGACAGAGAGAGCGGCTGTGTGC 60

Db	196	GTGCAGAAACACCCACCTTACCCCTGCGGGAGCGAGAGACAGGGGAGCGGCTGTGTGTC	255
Qy	61	GCCAGTGCSCCCCCAGGACCTTTGTGACGCGCGGTGCGCGAGACAGCCCCACGAGC	120
Db	256	GCCAGTGCSCCCCCAGGACCTTTGTGACGCGCGGTGCGCGAGACAGCCCCACGAGC	315
Qy	121	TGTGGCCGCTGTCCACGCGCCACTACACGAGTTCTGGAATCTACCTGGAGCGCTGCCGC	180
Db	316	TGTGGCCGCTGTCCACGCGCCACTACACGAGTTCTGGAATCTACCTAGAGCGCTGCCGC	375
Qy	181	TACTGCAACGCTCTCTGCGGGAGCGTAGGAGGACCGGCTTGCACGCGCACCCAC	240
Db	376	TACTGCAACGCTCTCTGCGGGAGCGTAGGAGGACCGGCTTGCACGCGCACCCAC	435
Qy	241	AACCGTGCCTGCCCTGCGGACCGGCTTCTTGCAGCAGCTGGTTCTGTCTTGAGGAC	300
Db	436	AACCGTGCCTGCCCTGCGGACCGGCTTCTTGCAGCAGCTGGTTCTGTCTTGAGGAC	495
Qy	301	GCATCGTGTCAACCTGTGCGGCGATTTGCCCGGGACACCCAGCCAGAACACGCG	360
Db	496	GCATCGTGTCAACCTGTGCGGCGATTTGCCCGGGACACCCAGCCAGAACACGCG	555
Qy	361	TGCAGCGCTGCCCCAGGACACCTTCTCAGCAGCAGCTCCAGCTCAGAGAGTCCGAG	420
Db	556	TGCAGCGCTGCCCCAGGACACCTTCTCAGCAGCAGCTCCAGCTCAGAGAGTCCGAG	615
Qy	421	CCCCACGCAACTGCAGCGCCCTGGGCTTGGCCCTCAATGTCCAGGCTCTTCTCCCAT	480
Db	616	CCCCACGCAACTGCAGCGCCCTGGGCTTGGCCCTCAATGTCCAGGCTCTTCTCCCAT	675
Qy	481	GACACCTGTGCACAGCTGACCTTCCCTCTCAGCACAGGGTACGAGGAGCTGAG	540
Db	676	GACACCTGTGCACAGCTGACCTTCCCTCTCAGCACAGGGTACGAGGAGCTGAG	735
Qy	541	GAGTGTAGCGTGCCTCATCGATTGTGGCTTTCAGAGACATCTCCATCAGAGGCTG	600
Db	736	GAGTGTAGCGTGCCTCATCGATTGTGGCTTTCAGAGACATCTCCATCAGAGGCTG	795
Qy	601	CAGCGCTGTGCAGGCGCTCGAGGCCCGGAGGGCTGGGGTCCGACCAAGGGCGGCG	660
Db	796	CAGCGCTGTGCAGGCGCTCGAGGCCCGGAGGGCTGGGGTCCGACCAAGGGCGGCG	855
Qy	661	CGCGGGCTTTGCAGCTGAAGCTCGCTCGGCGGCTCAGGAGCTCTCTGGGGCGCAGGAC	720
Db	856	CGCGGGCTTTGCAGCTGAAGCTCGCTCGGCGGCTCAGGAGCTCTCTGGGGCGCAGGAC	915
Qy	721	GGGGCGCTGTGCTGCGCTGCTCGAGCGCTGCGCTGGCCAGGATGCCCGGGCTGGAG	780
Db	916	GGGGCGCTGTGCTGCGCTGCTCGAGCGCTGCGCTGGCCAGGATGCCCGGGCTGGAG	975
Qy	781	CGGAGCTCCGTGAGCGCTTCTCCCTGTGCAC	813
Db	976	CGGAGCTCCGTGAGCGCTTCTCCCTGTGCAC	1008

Search completed: January 6, 2003, 14:40:26
Job time : 2682 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 6, 2003, 12:53:01 ; Search time 230 Seconds

(without alignments)
7960.324 Million cell updates/sec

Title: US-09-936-024-2

Perfect score: 813

Sequence: 1 ggcgcgaacaccacaccta.....agccttcctccctgcac 813

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues 4370478

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :
1: N.Geneseq.101002.*
2: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT.*
3: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT.*
4: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT.*
5: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT.*
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23: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001.DAT.*
24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	813	100.0	813	20	AAZ25377
2	813	100.0	813	21	AAZ25377
3	813	100.0	813	21	AAZ25377
4	813	100.0	813	21	AAZ25377
5	813	100.0	813	22	AAZ25377
6	813	100.0	813	24	AAZ25377
7	813	100.0	900	21	AAZ25377
8	813	100.0	900	21	AAZ25377
9	813	100.0	900	21	AAZ25377

10	813	100.0	903	20	AAZ25377	Orphan receptor (H
11	813	100.0	1055	22	AAZ25377	M68 TNF receptor
12	813	100.0	1066	22	AAZ25377	M68 TNF receptor
13	813	100.0	1077	19	AAZ25377	Human tumor necro
14	813	100.0	1077	21	AAZ25377	Human tumor necro
15	813	100.0	1077	24	AAZ25377	Human tumor necro
16	813	100.0	1114	21	AAZ25377	Human tumor necro
17	813	100.0	1114	21	AAZ25377	Human tumor necro
18	813	100.0	1114	21	AAZ25377	Human tumor necro
19	813	100.0	1114	21	AAZ25377	Human tumor necro
20	813	100.0	1114	22	AAZ25377	Human tumor necro
21	813	100.0	1114	22	AAZ25377	Human tumor necro
22	813	100.0	1164	19	AAZ25377	Human tumor necro
23	813	100.0	1168	20	AAZ25377	Human tumor necro
24	813	100.0	1179	22	AAZ25377	Human tumor necro
25	813	100.0	1205	20	AAZ25377	Human tumor necro
26	813	100.0	1347	21	AAZ25377	Human tumor necro
27	813	100.0	1428	21	AAZ25377	Human tumor necro
28	813	100.0	1462	20	AAZ25377	Human tumor necro
29	813	100.0	1462	20	AAZ25377	Human tumor necro
30	813	100.0	1462	20	AAZ25377	Human tumor necro
31	813	100.0	1462	20	AAZ25377	Human tumor necro
32	813	100.0	1462	20	AAZ25377	Human tumor necro
33	813	100.0	1462	20	AAZ25377	Human tumor necro
34	813	100.0	1462	20	AAZ25377	Human tumor necro
35	813	100.0	1462	20	AAZ25377	Human tumor necro
36	813	100.0	1462	20	AAZ25377	Human tumor necro
37	813	100.0	1462	20	AAZ25377	Human tumor necro
38	813	100.0	1462	20	AAZ25377	Human tumor necro
39	813	100.0	1462	20	AAZ25377	Human tumor necro
40	813	100.0	1462	20	AAZ25377	Human tumor necro
41	813	100.0	1462	20	AAZ25377	Human tumor necro
42	813	100.0	1462	20	AAZ25377	Human tumor necro
43	813	100.0	1462	20	AAZ25377	Human tumor necro
44	813	100.0	1462	20	AAZ25377	Human tumor necro
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ALIGNMENTS

RESULT 1	AAZ25377	standard; cDNA; 813 BP.
AC	AAZ25377	
XX	17-DEC-1999	(first entry)
XX	Human mFLINT #1 nucleotide sequence.	
XX	Human, FLINT, mFLINT, OPB3, tumour necrosis factor receptor, FasL,	
XX	apoptosis, inflammation; cancer; diabetes; acute liver failure;	
XX	sepsis; hepatitis; ischaemia-associated injury; hypercoagulation;	
XX	refusion-associated injury; aplastic anaemia; differentiation;	
XX	growth; myelodysplastic syndrome; pancytopenic condition;	
XX	myocardial ischaemia; ss.	
XX	Homo sapiens.	
XX	WO9950413-A2.	
XX	07-OCT-1999.	
XX	30-MAR-1999;	99WO-US06797.
XX	30-MAR-1998;	98US-0079856.
XX	20-MAY-1998;	98US-0086074.
XX	09-SEP-1998;	98US-0099643.
XX	17-DEC-1998;	98US-0112577.
XX	18-DEC-1998;	98US-0112703.
XX	18-DEC-1998;	98US-0112933.
XX	22-DEC-1998;	98US-0113407.

XX (ELIL) LILLY & CO ELI.
PI Bumol TF, Dou S, Glasebrook AL, Gould KE, Hale JE, Heuer JG;
PI Hui KY, Kharitonov A, Mizrahi J, Na S, Noblitt TW, Reidy CA;
PI Song HY, Wang J, Wu X, Zuckerman SH;
XX WPI; 1999-591319/50.
DR P-PSDB; AA242184.
XX
PT Use of mature FLINT for treating acute liver failure, inflammation,
PT cancer, and diabetes - by prevention of FasL-Fas mediated apoptotic
PT and proinflammatory activity
XX
XX Claim 29; Fig 3; 99pp; English.
XX
XX The present invention describes therapeutic applications of mature FLINT
CC (mFLINT) for use in the treatment of acute liver failure. Mature FLINT
CC (mFLINT), which is a member of the tumour necrosis factor receptor
CC superfamily, is used for treating acute liver failure, inflammation of
CC the liver, abnormal hepatocyte apoptosis, sepsis, a disorder associated
CC with inflammation, hepatitis, abnormal apoptosis, an ischaemia-associated
CC injury or disorder such as hypercoagulation (including use with
CC thrombolytic or anti-thrombolytic agents), reperfusion-associated injury
CC or disorder, type I diabetes, cancer, cell damage or damage to an
CC innocent bystander tissue that is induced by a chemotherapeutic agent or
CC therapeutic irradiation, treating haematopoietic progenitor cells that
CC have been exposed to therapeutic radiation or chemotherapy, aplastic
CC anaemia, myelodysplastic syndrome or a pancytopenic condition. mFLINT is
CC also used for promoting the growth or differentiation of a haematopoietic
CC progenitor cell or CD34+ cell and preventing damage to a cardiac myocyte
CC resulting from abnormal myocardial ischaemia. The present sequence
CC encodes human mFLINT.
XX
SQ Sequence 813 BP; 122 A; 298 C; 267 G; 126 T; 0 other;
Query Match 100.0%; Score 813; DB 20; Length 813;
Best Local Similarity 100.0%; Pred. No. 5.1e-145;
Matches 813; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTGGCAGAAACACCACTACCTGGCGGAGCGAGACAGGGAGCGGTGGTGC 60
Db 1 GTGGCAGAAACACCACTACCTGGCGGAGCGAGACAGGGAGCGGTGGTGC 60
QY 61 GCCCAGTGCCCGCCAGGACCTTTGTGACGCGCGGTGGCGGAGACAGCCACGACG 120
Db 61 GCCCAGTGCCCGCCAGGACCTTTGTGACGCGCGGTGGCGGAGACAGCCACGACG 120
QY 121 TGTGGCGCGTGTACCGCGCCATACACGACGTTCTGGAACTACCTGGAGCGCTGCCGC 180
Db 121 TGTGGCGCGTGTACCGCGCCATACACGACGTTCTGGAACTACCTGGAGCGCTGCCGC 180
QY 181 TACTGCAAGCTCTCTGCGGGAGCGGTGAGAGGAGCGAGCGGTGGCCACGCCAC 240
Db 181 TACTGCAAGCTCTCTGCGGGAGCGGTGAGAGGAGCGAGCGGTGGCCACGCCAC 240
QY 241 AACCGTGCTCGCGCTGCCGACCGGTCTTCTGCGCAGCGCTGTTCTCTTGGAGCAC 300
Db 241 AACCGTGCTCGCGCTGCCGACCGGTCTTCTGCGCAGCGCTGTTCTCTTGGAGCAC 300
QY 301 GCATGTGTCCATCTGTGCGCGGTGATTGCGCGGACACCCCGGACAGCAAGCAGCAG 360
Db 301 GCATGTGTCCATCTGTGCGCGGTGATTGCGCGGACACCCCGGACAGCAAGCAGCAG 360
QY 361 TGCAGCGGTGCGCCCGGACCTTCTCAGCCAGCAGCTCCAGCTCAGAGAGTCCAG 420
Db 361 TGCAGCGGTGCGCCCGGACCTTCTCAGCCAGCAGCTCCAGCTCAGAGAGTCCAG 420
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Db 481 GACACCTGTGCACAGCTGCACTGGCTTCCCTCAGCAGGATACAGGAGCTGAG 540
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Db 541 GAGTGTGAGCGTCCCGTCAATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG 600
QY 601 CAGCGGCTCTGAGGCGCTTCGAGGCGCCCGAGGGGTGGGTCCGACACCAAGGGCGGGC 660
Db 601 CAGCGGCTCTGAGGCGCTTCGAGGCGCCCGAGGGGTGGGTCCGACACCAAGGGCGGGC 660
QY 661 CCGCGCGGCTTCGAGCTGAAGCTGCGTGGCGGCTCACGAGCTCTGGGGGCGCAGGAC 720
Db 661 CCGCGGCGCTTCGAGCTGAAGCTGCGTGGCGGCTCACGAGCTCTGGGGGCGCAGGAC 720
QY 721 GGGGCGCTCTGCTGCGGCTGCTGCGAGGCGCTGCGGCTGGCCAGGATGCCCGGCTGGAG 780
Db 721 GGGGCGCTCTGCTGCGGCTGCTGCGAGGCGCTGCGGCTGGCCAGGATGCCCGGCTGGAG 780
QY 781 CGGAGCGTCCGTGAGGCGCTTCTCTCTGTCGAC 813
Db 781 CGGAGCGTCCGTGAGGCGCTTCTCTCTGTCGAC 813
RESULT 2
AAA75999
ID AAA75999 standard; DNA; 813 BP.
XX
AC AAA75999;
XX
DT 19-FEB-2001 (first entry)
XX
DE DNA encoding a mature human FAS Ligand Inhibitory Protein (FLINT).
XX
KW Human; FAS Ligand Inhibitory Protein; FLINT; analogue; apoptosis;
KW tumour necrosis factor receptor; acute lung injury; pulmonary fibrosis;
KW acute respiratory distress syndrome; ulcerative colitis;
KW chronic obstructive pulmonary disease; Crohn's disease; ss.
XX
OS Homo sapiens.
XX
PN WO200058465-A2.
XX
PD 05-OCT-2000.
XX
PF 20-MAR-2000; 2000WO-US06417.
XX
PR 30-MAR-1999; 99US-0126839.
PR 21-JUN-1999; 99US-0140077.
PR 21-JUN-1999; 99US-0140156.
PR 20-OCT-1999; 99US-0160566.
PR 18-FEB-2000; 2000US-0183398.
XX
XX (ELIL) LILLY & CO ELI.
XX
PI Becker GW, Cohen FU, Gonzalez-dewhitt PA, Hale JE, Micanovic R;
PI Newton CM, Noblitt TW, Rathmachalam R, Tschang SR, Witcher DR;
PI Wroblewski VJ;
XX
DR WPI; 2000-656167/63.
DR P-PSDB; AAB19334.
XX
PT FAS Ligand Inhibitory Protein analogs useful for treating abnormal
PT apoptosis related diseases e.g. acute lung injury, pulmonary fibrosis,
PT chronic obstructive pulmonary disease ulcerative colitis or Crohn's
PT disease
XX
PS Claim 37; Page 113; 114pp; English.
XX
XX The present sequence encodes a mature human FAS Ligand Inhibitory
CC Protein (FLINT). FLINT is a homologue of tumour necrosis factor receptor
CC proteins. FLINT inhibits the binding of FAS to FAS ligand. The mature
CC FLINT protein is modified to produce analogues, which have greater

CC potency, longer in vivo half-lives, decreased aggregation, decreased
 CC absorption onto surfaces, increased solubility and improved ease of
 CC formulation. The FLINT analogue is useful for treating a patient
 CC suffering from disease or condition relating to abnormal apoptosis such
 CC as acute lung injury, acute respiratory distress syndrome, pulmonary
 CC fibrosis, chronic obstructive pulmonary disease, ulcerative colitis, or
 CC Crohn's disease.

XX
 XX Sequence 813 BP; 122 A; 298 C; 267 G; 126 T; 0 other;

Query Match 100.0%; Score 813; DB 21; Length 813;
 Best Local Similarity 100.0%; Pred. No. 5.1e-145;

Matches 813; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGCAGAAACACCCACTTCTGCGGGAGGAGCAGAGACAGGGAGCGGCTGTGTGC 60
 DB 1 GTGGCAGAAACACCCACTTCTGCGGGAGGAGCAGAGACAGGGAGCGGCTGTGTGC 60
 QY 61 GCCCAGTGGCCCCCAGGACCTTTGTGACGCGCGCTGCGCGAGACAGCCCCAGCAGC 120
 DB 61 GCCCAGTGGCCCCCAGGACCTTTGTGACGCGCGCTGCGCGAGACAGCCCCAGCAGC 120
 QY 121 TGTGGCCCTGTGTCCACCGGCGCACTACAGAGTTCTTGAACTTACTTGAGCCGTGCC 180
 DB 121 TGTGGCCCTGTGTCCACCGGCGCACTACAGAGTTCTTGAACTTACTTGAGCCGTGCC 180
 QY 181 TACTGCAAGCTCTCTGCGGGGAGCGTGAAGAGGAGGACAGGGCTTGCACGCGCACCAC 240
 DB 181 TACTGCAAGCTCTCTGCGGGGAGCGTGAAGAGGAGGACAGGGCTTGCACGCGCACCAC 240
 QY 241 AACCGTGCCTGCGCGTCCGCGACGCGCTTCTTGCAGCAGCGTGGTTCTGTTGAGACAC 300
 DB 241 AACCGTGCCTGCGCGTCCGCGACGCGCTTCTTGCAGCAGCGTGGTTCTGTTGAGACAC 300
 QY 301 GCATGCTGTCCACTGTGTGCGCGGTGATTTGCCCGGACACCCCGACCAAGAACGCGAG 360
 DB 301 GCATGCTGTCCACTGTGTGCGCGGTGATTTGCCCGGACACCCCGACCAAGAACGCGAG 360
 QY 361 TGCAGCGCGTGGCCCCCAGGACCTTCTGAGCCAGCAGCTTCAGAGAGTGCAG 420
 DB 361 TGCAGCGCGTGGCCCCCAGGACCTTCTGAGCCAGCAGCTTCAGAGAGTGCAG 420
 QY 421 CCCACCGCACTGACAGGCGCTGGGCTGGGCTTCAATGTGACGAGCTTTCTCCCAT 480
 DB 421 CCCACCGCACTGACAGGCGCTGGGCTGGGCTTCAATGTGACGAGCTTTCTCCCAT 480
 QY 481 GACACCTGTGACACGACTGAGCTGGCTTCCCTCAGACACAGGATACCAAGAGCTGAG 540
 DB 481 GACACCTGTGACACGACTGAGCTGGCTTCCCTCAGACACAGGATACCAAGAGCTGAG 540
 QY 541 GAGTGTAGGCTGCGCTGATGATTTGTGCTTCCAGAGCATCTTCATCAAGAGCTG 600
 DB 541 GAGTGTAGGCTGCGCTGATGATTTGTGCTTCCAGAGCATCTTCATCAAGAGCTG 600
 QY 601 CAGCGGCTGTGACAGGCGCTGAGGCGCGGAGGAGGCTGGAGCTCCAGACCAAGGCGGAG 660
 DB 601 CAGCGGCTGTGACAGGCGCTGAGGCGCGGAGGAGGCTGGAGCTCCAGACCAAGGCGGAG 660
 QY 661 CGCGGCGCTTTGACGCTGAAGCTCGTGGGCGCTCAAGAGCTTCTGGGGGCGCAGAGC 720
 DB 661 CGCGGCGCTTTGACGCTGAAGCTCGTGGGCGCTCAAGAGCTTCTGGGGGCGCAGAGC 720
 QY 721 GGGGCGCTGTGTGCGGCTGTGACGCGCTGTGCGGTGGCAGAGATGCCGGGCTGAG 780
 DB 721 GGGGCGCTGTGTGCGGCTGTGACGCGCTGTGCGGTGGCAGAGATGCCGGGCTGAG 780
 QY 781 CGGAGCGCTGTGAGCGCTTCTCTCTGTGAC 813
 DB 781 CGGAGCGCTGTGAGCGCTTCTCTCTGTGAC 813

RESULT 3
 AAA88730

ID AAA88730 standard; cDNA; 813 BP.
 XX
 XX AAA88730;
 AC
 XX
 DT 05-FEB-2001 (first entry)
 XX
 XX Human FAS ligand inhibitor protein FLINT cDNA.
 DE
 XX
 XX FLINT; FAS ligand inhibitor protein; human; protease resistant;
 KW acute lung injury; acute respiratory distress syndrome;
 KW chronic obstructive pulmonary disease; pulmonary fibrosis;
 KW ulcerative colitis; therapy; organ transplantation; ss.
 XX
 XX Homo sapiens.
 OS
 XX
 XX MO200058466-A2.
 PN
 XX
 PD 05-OCT-2000.
 XX
 XX 20-MAR-2000; 2000MO-US06418.
 PF
 XX
 XX 30-MAR-1999; 99US-0126839.
 PR 21-JUN-1999; 99US-0140073.
 PR 04-AUG-1999; 99US-0147071.
 PR 20-OCT-1999; 99US-0160524.
 PR 21-OCT-1999; 99US-0160669.
 PR 20-DEC-1999; 99US-0172744.
 PR 26-JUN-2000; 2000US-0178184.
 XX
 XX (ELIL) LILLY & CO ELI.
 PA
 XX
 XX Micanovic R, Rathnachalam R, Witeher DR,
 PI
 XX
 XX WPI; 2000-664925/64.
 DR P-SDB; AAB19705.
 XX
 XX Novel protease resistant FAS ligand inhibitory protein analogues
 PT resistant to in vivo or in vitro proteolysis at amino acid position 218
 PT of the mature protein, useful for treating autoimmune diseases -
 PS disclosure; Page 95; 100pp; English.
 XX
 XX The present sequence is that of cDNA coding for human FAS ligand
 CC inhibitory protein FLINT mature protein (see AAB19705). FLINT is a
 CC tumour necrosis factor receptor homologue that binds FAS ligand.
 CC preventing its interaction with FAS. This interaction is implicated
 CC in runaway apoptosis and inflammatory disease. FLINT also binds to
 CC LIGHT, a membrane-bound ligand, which may play a role in immune
 CC modulation and apoptosis. The invention relates to novel FLINT
 CC analogues (see also AAB19706-09) that are resistant to proteolysis
 CC by trypsin-like proteases between positions 218 and 219 of the
 CC FLINT mature protein sequence. Nucleic acids, vectors and
 CC transformed host cells for recombinant production of the analogues
 CC are claimed. FLINT cDNA is used as a template for introducing the
 CC required point mutations e.g. via PCR mutagenesis. The protease
 CC resistant FLINT analogues are used to prevent or treat acute lung
 CC injury, acute respiratory stress syndrome, ulcerative colitis,
 CC chronic obstructive pulmonary disease, pulmonary fibrosis, to
 CC inhibit T lymphocyte activation, and to facilitate organ
 CC preservation for transplantation (claimed).
 CC
 XX
 XX Sequence 813 BP; 122 A; 298 C; 267 G; 126 T; 0 other;

Query Match 100.0%; Score 813; DB 21; Length 813;
 Best Local Similarity 100.0%; Pred. No. 5.1e-145;
 Matches 813; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGCAGAAACACCCACTTCTGCGGGAGGAGCAGAGACAGGGAGCGGCTGTGTGC 60
 DB 1 GTGGCAGAAACACCCACTTCTGCGGGAGGAGCAGAGACAGGGAGCGGCTGTGTGC 60
 QY 61 GCCCAGTGGCCCCCAGGACCTTTGTGACGCGCGCTGCGCGAGACAGCCCCAGCAGC 120

DB 61 GCCAGTGCCTCCAGGACCTTTGTGACGGCGGTGCGCGAGACAGACCCACGACG 120
QY 121 TGTGGCCCGTGTCAACCGCCCACTACACGAGTTCTGGAACCTACCTGGAGCGCTGCCGC 180
DB 121 TGTGGCCCGTGTCAACCGCCCACTACACGAGTTCTGGAACCTACCTGGAGCGCTGCCGC 180
QY 181 TACTGCAACGTCTCTGCGGGAGCGTGGAGGAGGACCGGCTTGCACGCCACCCAC 240
DB 181 TACTGCAACGTCTCTGCGGGAGCGTGGAGGAGGACCGGCTTGCACGCCACCCAC 240
QY 241 AACCGTGCCTGCCGCTGCCGACCGGCTTCTGCGCACGCTGTTCTGCTTTGGAGCAC 300
DB 241 AACCGTGCCTGCCGCTGCCGACCGGCTTCTGCGCACGCTGTTCTGCTTTGGAGCAC 300
QY 301 GCATCGTGTCCACTGTGTCGGCGTGAATGGCCCGGGACACCCCGAGCCAGAACAGCGAG 360
DB 301 GCATCGTGTCCACTGTGTCGGCGTGAATGGCCCGGGACACCCCGAGCCAGAACAGCGAG 360
QY 361 TGGCAGCGTGGCCCCCAGGACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCAG 420
DB 361 TGGCAGCGTGGCCCCCAGGACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCAG 420
QY 421 CCCACCGCAACTGCACGGCCCTGGGCTTGGCCCTCAATGTGCAGGCTCTTCTCCCAT 480
DB 421 CCCACCGCAACTGCACGGCCCTGGGCTTGGCCCTCAATGTGCAGGCTCTTCTCCCAT 480
QY 481 GACACCTGTGCAACGACTGCAGTGGCTTCCCTCAGCACACGAGGTACAGAGCTGAG 540
DB 481 GACACCTGTGCAACGACTGCAGTGGCTTCCCTCAGCACACGAGGTACAGAGCTGAG 540
QY 541 GAGTGTAGCGTCCGTCATGCTGCTTGTGGCTTCCAGGACATCTCCATCAGAGGCTG 600
DB 541 GAGTGTAGCGTCCGTCATGCTGCTTGTGGCTTCCAGGACATCTCCATCAGAGGCTG 600
QY 601 CAGCGGCTGTGACGGCCCTCGAGGCCCGAGGGCTGGGGTCCGACACCAAGGGCGGC 660
DB 601 CAGCGGCTGTGACGGCCCTCGAGGCCCGAGGGCTGGGGTCCGACACCAAGGGCGGC 660
QY 661 CGCGCGCTTGCAGCTGAAGTGCCTGCGCGGCTACAGAGCTCTTGGGGCGGAGGAC 720
DB 661 CGCGCGCTTGCAGCTGAAGTGCCTGCGCGGCTACAGAGCTCTTGGGGCGGAGGAC 720
QY 721 GGGCGCTGTGTCGGCTGCTCAGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGG 780
DB 721 GGGCGCTGTGTCGGCTGCTCAGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGG 780
QY 781 CGGAGCTGCGTGAAGCGCTTCCCTCCCTGTGCAC 813
DB 781 CGGAGCTGCGTGAAGCGCTTCCCTCCCTGTGCAC 813

RESULT 4
ID AAA51077
XX AAA51077 standard; DNA; 813 BP.
XX AC AAA51077;
XX DT 26-SEP-2000 (first entry)
XX DE Mature human FLINT coding sequence.
XX FLINT; osteoprotegrin 3; OP3; tumour necrosis factor receptor; TNFR;
KW FasL; LIGHT; apoptosis; pro-inflammatory; hepatotropic; vasotropic;
KW anti-diabetic; anti-anaemic; neuroprotective; anti-ulcer; cytostatic;
KW anti-inflammatory; antibacterial; immunosuppressive; ds.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
FT mat_peptide 1..813
FT /*tag= a
XX PN WO200037094-A2.

XX 29-JUN-2000.
XX PD 21-DEC-1999; 99WO-US30734.
XX PF 22-DEC-1998; 98US-0113407.
XX PR 30-MAR-1999; 99WO-US06797.
XX BR 20-OCT-1999; 99US-0172239.
XX XX (ELIL) LILLY & CO ELI.
XX Cohen FU, Posada JA, Wierda D;
XX WPI: 2000-475441/41.
XX P-PSDB; AAY96598.
XX Use of mature FLINT for treating e.g. acute respiratory distress
XX syndrome, ulcerative colitis or ischemic injury during organ
XX transplantation
XX Example 8; Fig 3A-B; 125pp; English.
XX Human FLINT (also known as osteoprotegrin 3) is a new tumour necrosis
XX factor receptor (TNFR) superfamily member, which binds FasL and LIGHT and
XX prevents FasL-Fas interaction. Mature FLINT (mFLINT) inhibits FasL-Fas
XX mediated apoptotic and pro-inflammatory activity. mFLINT is useful for
XX treating acute respiratory distress syndrome, treating or inhibiting
XX ulcerative colitis, inhibiting ischemic injury during organ
XX transplantation or for organ preservation during transplantation. mFLINT
XX can also be used to treat acute liver failure, inflammation of the liver,
XX abnormal (hepatocyte) apoptosis, sepsis, disorders associated with
XX inflammation, hepatitis, ischemia, hypercoagulation or reperfusion,
XX damage to a cardiac myocyte resulting from abnormal myocardial ischemia,
XX Type I diabetes, cancer, damage to an innocent bystander tissue induced
XX by a chemotherapeutic or therapeutic irradiation, aplastic anaemias,
XX myelodysplastic syndromes and pancytopenic conditions.
XX Sequence 813 BP; 122 A; 298 C; 267 G; 126 T; 0 other;
QY Query Match 100.0%; Score 813; DB 21; Length 813;
QY Best Local Similarity 100.0%; Pred. No. 5.1e-145;
QY Matches 813; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTGGCAGAAACACCCACCTACCCCTGGCGGAGCGAGACAGAGGAGCGGCTGGTGTGC 60
DB 1 GTGGCAGAAACACCCACCTACCCCTGGCGGAGCGAGACAGAGGAGCGGCTGGTGTGC 60
QY 61 GCCCAGTGCCTCCAGGACCTTTGTGACGGCGCTGCGCGGAGACAGACGCCCCACGACG 120
DB 61 GCCCAGTGCCTCCAGGACCTTTGTGACGGCGCTGCGCGGAGACAGACGCCCCACGACG 120
QY 121 TGTGGCCCGTGTCCACCGGCCACTACACGAGTTCTGGAACCTACCTGGAGCGCTGCCGC 180
DB 121 TGTGGCCCGTGTCCACCGGCCACTACACGAGTTCTGGAACCTACCTGGAGCGCTGCCGC 180
QY 181 TACTGCAACGTCTCTGCGGGAGCGTGGAGGAGGACCGGCTTGCACGCCACCCAC 240
DB 181 TACTGCAACGTCTCTGCGGGAGCGTGGAGGAGGACCGGCTTGCACGCCACCCAC 240
QY 241 AACCGTGCCTGCCGCTGCCGACCGGCTTCTGCGCACGCTGTTCTGCTTTGGAGCAC 300
DB 241 AACCGTGCCTGCCGCTGCCGACCGGCTTCTGCGCACGCTGTTCTGCTTTGGAGCAC 300
QY 301 GCATCGTGTCCACTGTGTCGGCGTGAATGGCCCGGGACACCCCGAGCCAGAACAGCGAG 360
DB 301 GCATCGTGTCCACTGTGTCGGCGTGAATGGCCCGGGACACCCCGAGCCAGAACAGCGAG 360
QY 361 TGGCAGCGTGGCCCCCAGGACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCAG 420
DB 361 TGGCAGCGTGGCCCCCAGGACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCAG 420
QY 421 CCCACCGCAACTGCACGGCCCTGGGCTTGGCCCTCAATGTGCAGGCTCTTCTCCCAT 480
DB 421 CCCACCGCAACTGCACGGCCCTGGGCTTGGCCCTCAATGTGCAGGCTCTTCTCCCAT 480

Db	421	CCCCACGGCAATGACAGGAGCCCTGGGAGCCCTCAATGATGCCAGGCTTTCTCCTCCAT	480
Qy	481	GACACCTCTGTGACCAAGTGTGACTGTGCTTCCCTCCACGACACAGGGTATCCAGAGCTGAG	540
Db	481	GACACCTCTGTGACCAAGTGTGACTGTGCTTCCCTCCACGACACAGGGTATCCAGAGCTGAG	540
Qy	541	GAGTGTAGCGGTGCGGTATGCACTTTGTGTGGCTTTCCAGACATCTCCATCAAGAGGCTG	600
Db	541	GAGTGTAGCGGTGCGGTATGCACTTTGTGTGGCTTTCCAGACATCTCCATCAAGAGGCTG	600
Qy	601	CAGCGGCTGCTGACAGAGCCCTGAGAGCCCGGAGAGGGAGTGGGGTCCGACACCAAGAGGCGGG	660
Db	601	CAGCGGCTGCTGACAGAGCCCTGAGAGCCCGGAGAGGGAGTGGGGTCCGACACCAAGAGGCGGG	660
Qy	661	CGCGGAGCTTGTGACGCTGAAGCTTGCCTGGAGCGAGCTCACGAGTCTCTGGGGGCGAGGAC	720
Db	661	CGCGGAGCTTGTGACGCTGAAGCTTGCCTGGAGCGAGCTCACGAGTCTCTGGGGGCGAGGAC	720
Qy	721	GGGGGCGCTGCTGTGTGTGCGGCTGCTGACAGGCGTGTGGCGTGGCCAGAGTATGCCCGGGCTGGAG	780
Db	721	GGGGGCGCTGCTGTGTGTGCGGCTGCTGACAGGCGTGTGGCGTGGCCAGAGTATGCCCGGGCTGGAG	780
Qy	781	CGGAGCGTTCGGTGAAGCGCTTCTCCCTGTGCAC	813
Db	781	CGGAGCGTTCGGTGAAGCGCTTCTCCCTGTGCAC	813

RESULT 5
AAD07380
ID AAD07380 standard; cDNA; 813 BP.

DT 04-AUG-2001 (first entry)

DE Human mature fas ligand inhibitory protein (FLINT) cDNA

KM human aas ligand inhibitory proteoin; FLINT; acute lung injury; ALI;
KM TNFR; tumour necrosis factor receptor proteoin; ulcerative colitis; ARDS
KM acute respiratory distress syndrome; pulmonary fibrosis; pr; therapy;
KM chronic obstructive pulmonary disease; COPD; acute lung injury; goitre;
KM rheumatoid arthritis; fibroproliferative lung disease; ischaemia; sepsis
KM fibrotic lung disease; human immunodeficiency virus; HIV; osteoporosis;
KM chronic renal failure; graft-vs-host disease; cutaneous inflammation;
KM vascular leak syndrome; Helicobacter pylori infection; atherosclerosis;
KM insulin dependent diabetes mellitus (IDDM); inflammatory bowel disease;
KM Crohn's disease; pancreatitis; cancer; autoimmune disease; psoriasis;
KM Down's syndrome; multiple sclerosis; cytostatic; neurologic;
KM neuroprotective; vasotrophic; ss.

OS Homo sapiens.

FH	Key	Location/Qualifiers
FT	CDS	1..813

```
FT /product= "Human mature fas ligand inhibitory protein  
FT (FLINT)"  
FT /note= "CDS does not include start and stop codon"  
FT /partial
```

PN WO200142463-A1.

PD 14-JUN-2001.

PF 29-NOV-2000; 2000WO-US30166.

PR 07-DEC-1999; 99US-0169367.

PR 07-DEC-1999; 99US-0169412.

PR 23-MAR-2000; 2000US-0191430.

PA (ELIL) LILLY & CO ELI.

XX

PI Lu J, Witcher DR;

DR WPI; 2001-381684/40.
DR P-PSDB; AAE03567.

DR P-PSDB; AAE03567.

PT New FLINT polypeptide for treating and/or preventing acute lung injury
PT acute respiratory distress syndrome, ulcerative colitis, and
PT graft-versus-host disease, comprises O-linked or N-linked.
PT oligosaccharides -

PS Example 1; Page 53; 60pp; English.

CC The present sequence is human mature fas ligand inhibitory protein
CC (FLINT) cDNA. FLINT, a homologue of tumour necrosis factor receptor
CC protein (TNFR), binds fas ligand (FasL) and thereby preventing the
CC interaction of FasL with fas. FLINT comprising O-linked or N-linked
CC oligosaccharides is useful for preventing or treating acute lung injury
CC (ALI), acute respiratory distress syndrome (ARDS), ulcerative colitis,
CC chronic obstructive pulmonary disease (COPD) and pulmonary fibrosis (PF),
CC to facilitate organ preservation for transplantation and to inhibit T
CC lymphocyte activation. FLINT is useful for treating and/or preventing
CC diseases such as rheumatoid arthritis, fibroproliferative lung disease,
CC fibrotic lung disease, acute lung injury, human immunodeficiency virus
CC (HIV), ischaemia, brain trauma/injury, chronic renal failure, graft-vs-
CC host disease, cutaneous inflammation, vascular leak syndrome,
CC Helicobacter pylori infection, goltire, atherosclerosis, insulin dependent
CC diabetes mellitus (IDDM), osteoporosis, inflammatory bowel disease,
CC Crohn's disease, sepsis, pancreatitis, cancer, autoimmune disease such as
CC psoriasis, Down's syndrome, and multiple sclerosis.

Sequence 813 BP; 122 A; 298 C; 267 G; 126 T; 0 other;

Query Match	100.0%;	Score 813;	DB 22;	Length 813;
-------------	---------	------------	--------	-------------

Matches 813; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGCAGAACACCCCACTACCCCTGGCGGACGCAGAGACAGGGAGCGGCTGGTGTGC 60

Db 1 GTGGCAGAAACACCCACCTACCCCTGGCGGACGCAGAGACAGGGAGCGGCTGGTGTGC 60

61 GCCCAGTCCCCCAGGACCTTTGTGCAAGCGCCGTGCCCGCGAGACAGCCCCACGACG 122

Db 61 GCCCAGTCCCCCCAGGCACTTGTGCA GCGGCCGTGCCGCCGAGACAGCCCAAGACG 12

QY 121 TGTGGCCCGTGTCCACCGCGCCACTACACGAGTTCTGGA CTACCTGGAGCGCTGCCG 180

Db 121 TGTGCCCGTGTCCACCGGCCACTACACGCAGTTCTGGACTACCTGAGCGCTGCCGC 18

QY 181 TACTGCAACGTCCTCTGCGGGAGCGTGAGGAGGACCGGCTTGCCACGCCACCCAC 24

Db 181 TACTGCAACGTCCTCTGCGGGAGCGTGAGGAGGACCGGCTTGCCACGCCACCCAC 24

QY 241 AACCGTGCCTGCCGCTGCCGACCGGCTTCTTCGGCGACGCTGGTTCTGCTTGAAC 30

Db 241 AACCGTGCCTGCCGCTGCGCACCGGCTTCTTCGCGCACGCTGTTTCTGCTTGAGCAC 30

301 GCATCGTTCACCTGGTGCCGGCGTGATTGCCCGGGACCCCGAGCCAGAACACGCAG 360

Db 301 GCATCGTCCACCTGTGCCGGCGTGATTGCCCGGGCACCCCAAGCCAGAACACGCAG 36

QY 361 TGGCAGCCGTGCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 422

Db 361 TGGCAGCCGTGCCCCCAGGCACTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 42

421 CCCACCGCACTGCACGGCCCTGGGCTGGCCCTCATATGTGCCAAGGCTTCTCCCAT 48

Db 421 CCCACCGCACTGCACGGCCCTGGGCTGCCCTCATGTGCCAGGCTCTTCTCCCAT 48

QY 481 GACACCTGTGCACCAGCTGCACCTGGCTTCCCCCTCAGCACCAAGGTACCAGGAGCTGAG 54

Db 481 GACACCCCTGTGACACGAGCTGCTTCCCCCTCAGCACCAAGGTTACCAAGAGCTGAG 54

541 GAGTGTGAGCGTGCCGTCATCGACTTGTGGCTTTCAGGACATCTCCATCAAGAGGCTG 60

||||| 541 GAGTGTGAGCGTCCGTCATCGACTTTGTGCTTTCAGAGACATCTCCATCAAGAGCTG 600
Db
601 CAGCGGCTGTGACAGGCTTCGAGGCCCCGAGGCTGGGGTCCGACACCAAGGGCGGC 660
QY
601 CAGCGGCTGTGACAGGCTTCGAGGCCCCGAGGCTGGGGTCCGACACCAAGGGCGGC 660
Db
661 CGCGCGCTTTGACGTGAAGCTGCGTGGCGGCTACGAGCTCTGGGGGCGGAGAC 720
QY
661 CGCGCGCTTTGACGTGAAGCTGCGTGGCGGCTACGAGCTCTGGGGGCGGAGAC 720
Db
721 GCGCGCTGTGCTGCGGCTGCGAGGCTGCGGCTGCGAGGATGCCCGGCTGGAG 780
QY
721 GCGCGCTGTGCTGCGGCTGCGAGGCTGCGGCTGCGAGGATGCCCGGCTGGAG 780
Db
781 CGGAGCTCCGTGAGCGCTTCTCCCTGTGCAC 813
Db
781 CGGAGCTCCGTGAGCGCTTCTCCCTGTGCAC 813
Db
RESULT 6
AAD27868
ID AAD27868 standard; DNA; 813 BP.
XX
AC AAD27868;
XX
01-JUL-2002 (first entry)
XX
DT Human mature FLINT DNA.
XX
DE
XX
KW FLINT; FAS ligand inhibitory protein; pulmonary; lung; apoptosis;
KW organ failure; liver; kidney; pancreas; inflammatory disease;
KW neutrophil; sepsis; acute respiratory distress syndrome;
KW acute lung injury; systemic inflammatory response syndrome; SIRS;
KW multiple organ dysfunction; MODS; human; gene; ds.
XX
OS Homo sapiens.
XX
Key Location/Qualifiers
FH 1..813
FT CDS /tag= a
FT /product= "Mature FLINT protein"
FT /note= "Does not include start and stop codons"
FT /partial
XX
PN WO200209668-A2.
XX
PD 07-FEB-2002.
XX
PF 20-JUL-2001; 2001WO-US21105.
XX
PR 02-AUG-2000; 2000US-222476P.
XX
PA (ELIL) LILLY & CO ELI.
XX
XX Micranovic R, Witcher DR;
XX WPI; 2002-206149/26.
XX P-PSDB; AAE14578.
XX
XX Administering FLINT (FAS ligand inhibitory protein) or FLINT analog,
PT useful for treating e.g. sepsis or respiratory distress syndrome,
PT involves pulmonary administration of a therapeutic amount of the FLINT
PT or FLINT analog -
XX
XX Disclosure; Page 30; 35pp; English.
XX
XX The invention relates to a new method of administering FLINT
CC (FAS ligand inhibitory protein) or FLINT analog that involves pulmonary
CC administration of a therapeutic amount of the FLINT or FLINT analog.
CC The method enables systemic absorption of FLINT through lungs and
CC significantly reduces or eliminates the need for administering FLINT by
CC injection or other routes of administration. The method is useful in

CC treating disorders related to enhanced apoptosis (e.g. organ failure
CC in liver, kidneys and pancreas) and inflammatory diseases associated with
CC neutrophil activation (e.g. sepsis, acute respiratory distress syndrome,
CC acute lung injury, systemic inflammatory response syndrome (SIRS) and
CC multiple organ dysfunction (MODS)). The method minimises the pain
CC and discomfort of injection methods. The present sequence is human
CC mature FLINT DNA.
XX
SQ Sequence 813 BP; 122 A; 298 C; 267 G; 126 T; 0 other;
Query Match 100.0%; Score 813; DB 24; Length 813;
Best Local Similarity 100.0%; Pred. No. 5.1e-145;
Matches 813; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTGGCAGAAACACCCACCTTACCCCTGGCGGACGACAGACAGAGGCGGTGGTGTGC 60
Db 1 GTGGCAGAAACACCCACCTTACCCCTGGCGGACGACAGACAGAGGCGGTGGTGTGC 60
QY 61 GCCAGTGCCTCCAGGACCTTTGTGAGCGGCGTGGCGGACAGCCAGCG 120
Db 61 GCCAGTGCCTCCAGGACCTTTGTGAGCGGCGTGGCGGACAGCCAGCG 120
QY 121 TGTGGCCCGTGTCCACCGGCCACTACACGCACTTCTGGAATACCTGGAGCGCTGCCG 180
Db 121 TGTGGCCCGTGTCCACCGGCCACTACACGCACTTCTGGAATACCTGGAGCGCTGCCG 180
QY 181 TACTGCAACGCTCTCTGCGGGAGCGTGGAGGAGGACGCGGCTTGCACGCCAC 240
Db 181 TACTGCAACGCTCTCTGCGGGAGCGTGGAGGAGGACGCGGCTTGCACGCCAC 240
QY 241 AACCGTGCCTGCGGCTGCGCACCGGCTTCTTCGCGCAGCGCTTCTGCTTGGAGCAC 300
Db 241 AACCGTGCCTGCGGCTGCGCACCGGCTTCTTCGCGCAGCGCTTCTGCTTGGAGCAC 300
QY 301 GCATCTGTCCACCTGGTGCCTGCGGCGTATTGCCCGGCGGACCCCGAGCAGACGCG 360
Db 301 GCATCTGTCCACCTGGTGCCTGCGGCGTATTGCCCGGCGGACCCCGAGCAGACGCG 360
QY 361 TGCACGCGTGCCTCCCGAGGACCTTCTCAGCGAGAGCTTCCAGCTCAGAGCTGCCAG 420
Db 361 TGCACGCGTGCCTCCCGAGGACCTTCTCAGCGAGAGCTTCCAGCTCAGAGCTGCCAG 420
QY 421 CCCACGCGCAACTGCACGCGCTTGGCGCTTGGCGCTCAATGTGCGAGGCTTCTCCCAT 480
Db 421 CCCACGCGCAACTGCACGCGCTTGGCGCTTGGCGCTCAATGTGCGAGGCTTCTCCCAT 480
QY 481 GACACCTGTGCACACGCTGCATGGCTTCCCCTCAGCACACAGGCTTACAGGAGCTGAG 540
Db 481 GACACCTGTGCACACGCTGCATGGCTTCCCCTCAGCACACAGGCTTACAGGAGCTGAG 540
QY 541 GAGTGTGAGCGTGCCTCATTCGACTTTTGGCTTTCAGGACATCTCCATCAAGAGGCTG 600
Db 541 GAGTGTGAGCGTGCCTCATTCGACTTTTGGCTTTCAGGACATCTCCATCAAGAGGCTG 600
QY 601 CAGCGGCTGTGAGCGCTTCCGAGGCGGCTGGGGTCCGACACCAAGGGCGGC 660
Db 601 CAGCGGCTGTGAGCGCTTCCGAGGCGGCTGGGGTCCGACACCAAGGGCGGC 660
QY 661 CGCGCGCTTGTGAGCTGAAGCTGCGTGGCGGCTCACGAGCTCTGGGGGCGGAGAC 720
Db 661 CGCGCGCTTGTGAGCTGAAGCTGCGTGGCGGCTCACGAGCTCTGGGGGCGGAGAC 720
QY 721 GCGCGCTGTGCTGCGGCTGCTGAGGCGCTGCGGCTGCGAGGATGCCCGGCTGGAG 780
Db 721 GCGCGCTGTGCTGCGGCTGCTGAGGCGCTGCGGCTGCGAGGATGCCCGGCTGGAG 780
QY 781 CGGAGCTCCGTGAGCGCTTCTCCCTGTGCAC 813
Db 781 CGGAGCTCCGTGAGCGCTTCTCCCTGTGCAC 813
Db
RESULT 7
AA225375

XX AA25375 standard; cDNA; 900 BP.
XX AA25375;
XX 17-DEC-1999 (first entry)
XX Human FLINT #1 nucleotide sequence.
XX Human FLINT; mFLINT; OPG3; tumour necrosis factor receptor; FasL;
XX apoptosis; inflammation; cancer; diabetes; acute liver failure;
XX sepsis; hepatitis; ischaemia-associated injury; hypercoagulation;
XX reperfusion-associated injury; aplastic anaemia; differentiation;
XX growth; myelodysplastic syndrome; pancytopenic condition;
XX myocardial ischaemia; ss.
XX Homo sapiens.
XX W09950413-A2.
XX 07-OCT-1999.
XX 30-MAR-1999; 99WO-US06797.
XX 30-MAR-1998; 98US-0079856.
XX 20-MAY-1998; 98US-0086074.
XX 09-SEP-1998; 98US-0099643.
XX 17-DEC-1998; 98US-0112577.
XX 18-DEC-1998; 98US-0112703.
XX 18-DEC-1998; 98US-0112933.
XX 22-DEC-1998; 98US-0113407.
XX (ELIL) LILLY & CO ELI.
XX Bimol TF, Dou S, Glaesbrook AL, Gould KE, Hale UF, Heuer JG;
XX Hui KY, Kharitonov A, Mizrahi J, Na S, Noblitt TW, Reidy CA;
XX Song HY, Wang J, Wu X, Zuckerman SH;
XX WPI: 1999-591319/50.
XX P-PsDB; AAY42182.
XX Use of mature FLINT for treating acute liver failure, inflammation,
XX cancer, and diabetes - by prevention of FasL-Fas mediated apoptotic
XX and proinflammatory activity
XX Claim 28; Fig 1; 99pp; English.
XX The present invention describes therapeutic applications of mature FLINT
XX (mFLINT) for use in the treatment of acute liver failure. Mature FLINT
XX (mFLINT), which is a member of the tumour necrosis factor receptor
XX superfamily, is used for treating acute liver failure, inflammation of
XX the liver, abnormal hepatocyte apoptosis, sepsis, a disorder associated
XX with inflammation, hepatitis, abnormal apoptosis, an ischaemia-associated
XX injury or disorder such as hypercoagulation (including use with
XX thrombolytic or anti-thrombolytic agents), reperfusion-associated injury
XX or disorder, Type I diabetes, cancer, cell damage or damage to an
XX innocent bystander tissue that is induced by a chemotherapeutic agent or
XX therapeutic irradiation, treating haematopoietic progenitor cells that
XX have been exposed to therapeutic radiation or chemotherapy, aplastic
XX anaemia, myelodysplastic syndrome or a pancytopenic condition. mFLINT is
XX also used for promoting the growth or differentiation of a haematopoietic
XX progenitor cell or CD34+ cell and preventing damage to a cardiac myocyte
XX resulting from abnormal myocardial ischaemia. The present sequence
XX encodes human FLINT.
XX
SQ Sequence 900 BP; 128 A; 324 C; 304 G; 144 T; 0 other;
Query Match 100.0%; Score 813; DB 20; Length 900;
Best Local Similarity 100.0%; Pred. No. 5, 1e-145;
Matches 813; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX 1 GTGGCAGAAACACCCACTTACCTGCGGAGCAGACAGACAGGAGGAGGCTGTGTGC 60
XX GTGGCAGAAACACCCACTTACCTGCGGAGCAGACAGACAGGAGGAGGCTGTGTGC 60
XX 88 GTGGCAGAAACACCCACTTACCTGCGGAGCAGACAGACAGGAGGAGGCTGTGTGC 147

XX 61 GCCCAGTGCCTCCCGAGGACCTTTGTGAGGCGCGTGCAGGAGAGCCCGACAGAC 120
XX 148 GCCCAGTGCCTCCCGAGGACCTTTGTGAGGCGCGTGCAGGAGAGCCCGACAGAC 207
XX 121 TGTGAGCCCGTGTCCACCGCGCACTACACGAGTTCTGAACTACGAGCGTGCAGC 180
XX 208 TGTGAGCCCGTGTCCACCGCGCACTACACGAGTTCTGAACTACGAGCGTGCAGC 267
XX 181 TACTGCAACGTCCTCTGTGAGGAGCGTGAAGAGAGAGGAGCGGCTTGCACGCCAC 240
XX 268 TACTGCAACGTCCTCTGTGAGGAGCGTGAAGAGAGGAGCGGCTTGCACGCCAC 327
XX 241 AACCGTGCCTGCGCTGCGGACCGGCTTCTGCGGACGCTGTTCTGTGAGAGAC 300
XX 328 AACCGTGCCTGCGCTGCGGACCGGCTTCTGCGGACGCTGTTCTGTGAGAGAC 387
XX 301 GCATCGTGTCCACCTGTGTGCGGCGTATTCGCCGAGCAACCCACGACGACGACG 360
XX 388 GCATCGTGTCCACCTGTGTGCGGCGTATTCGCCGAGCAACCCACGACGACGACG 447
XX 361 TGCCAGCCGTGCCCCCGAGGACCTTCTCAGCCAGCAGCTTCAGCTAGAGAGTCCAG 420
XX 448 TGCCAGCCGTGCCCCCGAGGACCTTCTCAGCCAGCAGCTTCAGCTAGAGAGTCCAG 507
XX 421 CCCGACCGCAACCTGACAGGCGCTGCGGCGTGCAGTCCCAATGTCGACGCTTCTCCCAT 480
XX 508 CCCGACCGCAACCTGACAGGCGCTGCGGCGTGCAGTCCCAATGTCGACGCTTCTCCCAT 567
XX 481 GACACCTGTGTGCAACGAGCTGACCTGCTCCCTCAGCAGCAGAGGTAACAGAGCTGAG 540
XX 568 GACACCTGTGTGCAACGAGCTGACCTGCTCCCTCAGCAGCAGAGGTAACAGAGCTGAG 627
XX 541 GAGTGTGAGCTGCGCTGATGACCTTGTGCTTCCAGGACATTCATCAGAGGCTG 600
XX 628 GAGTGTGAGCTGCGCTGATGACCTTGTGCTTCCAGGACATTCATCAGAGGCTG 687
XX 601 CAGGCGCTGTGTCAGGCGCTGACGCGCCCGAGGCGTGGGTCCGACACCAAGGCGCGG 660
XX 688 CAGGCGCTGTGTCAGGCGCTGACGCGCCCGAGGCGTGGGTCCGACACCAAGGCGCGG 747
XX 661 CGCGCGCTGTGTCAGGCGCTGACGCGCGCTGACGAGCTCTGTGGGCGCAGAGAC 720
XX 748 CGCGCGCTGTGTCAGGCGCTGACGCGCGCTGACGAGCTCTGTGGGCGCAGAGAC 807
XX 721 GGGGCGCTGTGTCAGGCGCTGACGCGCGCTGACGAGCTGCGCGAGATGCCGCGCTGAG 780
XX 808 GGGGCGCTGTGTCAGGCGCTGACGCGCGCTGACGAGCTGCGCGAGATGCCGCGCTGAG 867
XX 781 CGGAGCGTGTGTCAGGCGCTTCTCCCTGTGCAC 813
XX 868 CGGAGCGTGTGTCAGGCGCTTCTCCCTGTGCAC 900
XX
XX RESULT 8
XX ID AAAS3208 standard; cDNA; 900 BP.
XX AAAS3208;
XX AAAS3201 (first entry)
XX 03-JAN-2001
XX Human Fas ligand inhibitor FLINT coding sequence.
XX Human, Fas ligand inhibitor; FLINT; apoptosis; autoimmune disease;
XX inflammation; infectious disease; ischaemia; Alzheimer's disease;
XX Parkinson's disease; Crohn's disease; transplantation; ss.
XX Homo sapiens.
XX Key Location/Qualifiers
XX CDS 1..900
XX FT
XX /tag= a

FT /product= "FLINT"
FT /partial
FT 1..90
FT /tag= b
FT mat_peptide 91..900
FT /tag= c
XX

WO200034782-A1.

15-JUN-2000.

07-DEC-1999; 99WO-US28696.

09-DEC-1998; 98US-0111575.

09-DEC-1998; 98US-0111580.

07-JAN-1999; 99US-0115069.

(ELIL) LILLY & CO ELI.

Rostock PRJ, Song HY, Su EW;

WPI; 2000-431379/37.

P-PSDB; AAB03621.

Novel monkey Fas ligand inhibitor polypeptides, useful for treating inflammatory or autoimmune disease such as rheumatoid arthritis, infectious diseases such as chronic hepatitis, and

Ischaemia/Re-perfusion conditions -

Example 1; Page 88-91; 101pp; English.

The present sequence is the coding sequence of the human Fas ligand inhibitor (FLINT). The FLINT protein is involved in cell-specific apoptosis, and can be used to treat inflammatory and autoimmune diseases such as rheumatoid arthritis, inflammatory bowel disease, graft-versus-host disease, diabetes, psoriasis and Graves' disease, infectious diseases such as HIV-induced lymphopenia, fulminant viral hepatitis B/C, chronic hepatitis and cirrhosis, and H. pylori-associated ulceration, ischaemia and reperfusion conditions including acute myocardial infarction, acute coronary syndrome, congestive heart failure and atherosclerosis, and Alzheimer's and Parkinson's diseases, brain injury and acute respiratory distress syndrome, Crohn's disease, aplastic trauma and injury, chronic glomerulonephritis, osteoporosis, aneemia, myelodysplasia, ulcerative colitis, Down's syndrome, and multiple sclerosis. In addition, the gene and protein can be used to prevent apoptosis following organ transplantation.

Sequence 900 BP; 128 A; 324 C; 304 G; 144 T; 0 other;

Query Match 100.0%; Score 813; DB 21; Length 900;

Best Local Similarity 100.0%; Pred. No. 5.1e-145;

Matches 813; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCAGAAACCCACTACCTCCCTGGCGGACGACAGACAGGGAGCGGTGGTGC 60

DB 88 GTGCAGAAACCCACTACCTCCCTGGCGGACGACAGACAGGGAGCGGTGGTGC 147

QY 61 GCCCAGTGCCCCCAGGACCTTTGTGAGCGGCGCGCCGAGACAGCCCCACGACG 120

DB 148 GCCCAGTGCCCCCAGGACCTTTGTGAGCGGCGCGCGCCGAGACAGCCCCACGACG 207

QY 121 TGTGGCCCGTGTCCACCGCGCCACTACACGAGTTCTGGAACTACCTGGAGCGGTGCCGC 180

DB 208 TGTGGCCCGTGTCCACCGCGCCACTACACGAGTTCTGGAACTACCTGGAGCGGTGCCGC 267

QY 181 TACTGCAACGTCTCTCGGGGAGCGTGGAGAGAGGACGGGCTTCCACGCGCCAC 240

DB 268 TACTGCAACGTCTCTCGGGGAGCGTGGAGAGAGGACGGGCTTCCACGCGCCAC 327

QY 241 AACCGTCCGTGCGCGTCCGCGACCGGCTTCTTCGCGACCGTGGTTTCTGTTGGAGCAC 300

DB 328 AACCGTCCGTGCGCGTCCGCGACCGGCTTCTTCGCGACCGTGGTTTCTGTTGGAGCAC 387

QY 301 GCATCGTGTCCACCTGGTCCGCGGTGATTGCCCGGGCACCCCGAGCAGAACGCGAG 360
DB 388 GCATCGTGTCCACCTGGTCCGCGGTGATTGCCCGGGCACCCCGAGCAGAACGCGAG 447
QY 361 TGCACGCGGTGCCCGCCAGGACCTTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTCCAG 420
DB 448 TGCACGCGGTGCCCGCCAGGACCTTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTCCAG 507
QY 421 CCCACCGCAACTGCACGCGCCCTGGGCTTCCGCTCAATGTGCGAGGCTCTTCTCCCAT 480
DB 508 CCCACCGCAACTGCACGCGCCCTGGGCTTCCGCTCAATGTGCGAGGCTCTTCTCCCAT 567
QY 481 GACACCTGTGCACGAGCTGCCTGGCTTCCGCTCAGCAGCAGGCTACGAGGAGTGGAG 540
DB 568 GACACCTGTGCACGAGCTGCCTGGCTTCCGCTCAGCAGCAGGCTACGAGGAGTGGAG 627
QY 541 GAGTGTGAGCGTGCCTCATCGACTTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG 600
DB 628 GAGTGTGAGCGTGCCTCATCGACTTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG 687
QY 601 CAGCGCTGTGCAGGCGCTTCGAGGCGCCGAGGCGTGGGTCGACACCAAGGGCGGGC 660
DB 688 CAGCGCTGTGCAGGCGCTTCGAGGCGCCGAGGCGTGGGTCGACACCAAGGGCGGGC 747
QY 661 CCGCGCGCTTGCAGCTGAAGCTGCGTGGCGGCTCAGGAGCTCCTGGGGCGCAGGAC 720
DB 748 CCGCGCGCTTGCAGCTGAAGCTGCGTGGCGGCTCAGGAGCTCCTGGGGCGCAGGAC 807
QY 721 GGGCGCTGTGTGGCGCTGTGCGAGGCGCTGCGGCTGGCCAGGATGCCCGGCTGGAG 780
DB 808 GGGCGCTGTGTGGCGCTGTGCGAGGCGCTGCGGCTGGCCAGGATGCCCGGCTGGAG 867
QY 781 CCGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 813
DB 868 CCGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 900

RESULT 9

AAA51075
ID AAA51075 standard; DNA; 900 BP.

AC AAA51075;

XX 26-SEP-2000 (first entry)

DT Human FLINT coding sequence.

DE

XX FLINT; osteoprotegerin 3; OPG3; tumour necrosis factor receptor; TNFR;

XX FastL; LIGHT; apoptosis; pro-inflammatory; hepatotropic; vasotropic;

XX anti-diabetic; anti-anaemic; neuroprotective; anti-ulcer; cytostatic;

XX anti-inflammatory; antibacterial; immunosuppressive; ds.

OS Homo sapiens.

XX Key Location/Qualifiers

FT CDS 1..900

FT /tag= a

FT /product= FLINT

FT /partial

FT sig_peptide 1..87

FT /tag= b

FT mat_peptide 88..900

FT /tag= c

XX WO200037094-A2.

XX 29-JUN-2000.

XX 21-DEC-1999; 99WO-US30734.

XX 22-DEC-1998; 98US-0113407.

XX 30-MAR-1999; 99WO-US06797.

XX 20-OCT-1999; 99US-0172239.

XX (ELIL) LILLY & CO ELI.
 XX Cohen Fu, Posada JA, Wierda D;
 PI WPI: 2000-475441/41.
 XX P-PSDB; AAY96596.
 DR
 XX Use of mature FLINT for treating e.g. acute respiratory distress
 PT syndrome, ulcerative colitis or ischemic injury during organ
 PT transplantation
 XX
 PS Example 7, Fig 1A-B; 125pp; English.
 XX
 CC Human FLINT (also known as osteoprotegerin 3) is a new tumour necrosis
 CC factor receptor (TNFR) superfamily member, which binds FasL and LIGHT and
 CC prevents FasL-Fas interaction. Mature FLINT (mFLINT) inhibits FasL-Fas
 CC mediated apoptotic and pro-inflammatory activity. mFLINT is useful for
 CC treating acute respiratory distress syndrome, treating or inhibiting
 CC ulcerative colitis, inhibiting ischemic injury during organ
 CC transplantation or for organ preservation during transplantation. mFLINT
 CC can also be used to treat acute liver failure, inflammation of the liver,
 CC abnormal (hepatocyte) apoptosis, sepsis, disorders associated with
 CC inflammation, hepatitis, ischemia, hypercoagulation or reperfusion,
 CC damage to a cardiac myocyte resulting from abnormal myocardial ischaemia,
 CC Type 1 diabetes, cancer, damage to an innocent bystander tissue induced
 CC by a chemotherapeutic or therapeutic irradiation, aplastic anaemias,
 CC myelodysplastic syndromes and pancytopenic conditions.
 XX
 XX Sequence 900 BP; 128 A; 324 C; 304 G; 144 T; 0 other;
 SO
 Query Match 100.0%; Score 813; DB 21; Length 900;
 Best Local Similarity 100.0%; Pred. No. 5.1e-145;
 Matches 813; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 628 GAGTGTAGGCGCCGTCATCGACTTTGTGGCTTTCAGGACATCTCCATCAAGGCTG 687
 QY 601 CAGCGCTGTGAGGCGCCCTCGAGGCGCCGAGAGGCTCGGAGTCCGACACCAAGGCGGC 660
 DB 688 CAGCGCTGTGAGGCGCCCTCGAGGCGCCGAGAGGCTCGGAGTCCGACACCAAGGCGGC 747
 QY 661 CCGCGGCGCTTGGAGCTGAAGCTGCGCGGCTCGACGAGCTCTGGGGGCGCAGAGC 720
 DB 748 CCGCGGCGCTTGGAGCTGAAGCTGCGCGGCTCGACGAGCTCTGGGGGCGCAGAGC 807
 QY 721 GGGGCGCTGTGCTGTGCGGCTGTGCGAGCGCTCGCGGTGCGCAGATGCCGGGCTGGAG 780
 DB 808 GGGGCGCTGTGCTGTGCGGCTGTGCGAGCGCTCGCGGTGCGCAGATGCCGGGCTGGAG 867
 QY 781 CGGAGCGTCCGTGAGGCGCTTCCCTCGTGCAC 813
 DB 868 CGGAGCGTCCGTGAGGCGCTTCCCTCGTGCAC 900
 RESULT 10
 AAX22300
 ID AAX22300 standard; DNA; 903 BP.
 XX
 AC AAX22300;
 XX
 DT 20-MAY-1999 (first entry)
 XX
 DE Orphan receptor (HUMAN NTR-1) polypeptide encoding DNA.
 XX
 XX HUMAN NTR-1; orphan receptor; osteoprotegerin; OPG; TNFR; human;
 KW tumour necrosis factor receptor; muscle disorder; bone mass; screening;
 KM muscle metabolism; binding agent; cognate ligand; ss.
 XX
 OS Homo sapiens.
 XX
 PN MO9907738-A2.
 XX
 PD 18-FEB-1999.
 XX
 PF 04-AUG-1998; 98WO-US16202.
 XX
 PR 06-AUG-1997; 97US-0054869.
 XX
 PA (PROC) PROCTER & GAMBLE CO.
 PA (REG-) REGENERON PHARM INC.
 XX
 PI Maslakowski PJ, Morris J, Valenzuela DM;
 DR WPI: 1999-167365/14.
 DR P-PSDB; AAW5082.
 XX
 PT Novel orphan human receptor polypeptide and nucleic acid - useful as
 PT diagnostic reagents and for treatment of muscle disorders
 XX
 PS Claim 2; Page 21; 23pp; English.
 XX
 CC This DNA encodes a HUMAN NTR-1 polypeptide, a novel orphan receptor. The
 CC protein is related to osteoprotegerin (OPG) and to tumour necrosis factor
 CC receptor (TNFR). Host cells transformed with a vector comprising the
 CC HUMAN NTR-1 nucleic acid are used for the recombinant expression of the
 CC protein. HUMAN NTR-1 proteins and antibodies immuno specific for the
 CC protein are useful for diagnosis and treatment of humans and animals,
 CC especially muscle disorders, as the receptor is involved in regulation of
 CC bone mass and muscle metabolism. HUMAN NTR-1 receptors are also useful
 CC for screening for novel binding agents, and cognate ligands, which may be
 CC used to treat disorders associated with HUMAN NTR-1 imbalance.
 XX
 SO Sequence 903 BP; 129 A; 324 C; 305 G; 145 T; 0 other;
 Query Match 100.0%; Score 813; DB 20; Length 903;
 Best Local Similarity 100.0%; Pred. No. 5.1e-145;
 Matches 813; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCGAGAAACACCCACCTTACCCCTGGGGGAGCCAGAGACAGGGAGCGGCTGGTGTGC 60
Db 88 GTGCGAGAAACACCCACCTTACCCCTGGGGGAGCCAGAGACAGGGAGCGGCTGGTGTGC 147
QY 61 GCCCAGTGCCTCCAGAGCAGCTTTGTGAGCGGCGCTGGCGCGAGACAGCCCAACGACG 120
Db 148 GCCCAGTGCCTCCAGAGCAGCTTTGTGAGCGGCGCTGGCGCGAGACAGCCCAACGACG 207
QY 121 TGTGGCGCTGTCCACCGCGCACTACACGAGTTCTGGAACTACCTGGAGCGCTGCCGC 180
Db 208 TGTGGCGCTGTCCACCGCGCACTACACGAGTTCTGGAACTACCTGGAGCGCTGCCGC 267
QY 181 TACTGCAACGCTCTCTGCGGGAGCGTGAAGAGAGGCAAGGGCTTGCAGCGCCACCCAC 240
Db 268 TACTGCAACGCTCTCTGCGGGAGCGTGAAGAGAGGCAAGGGCTTGCAGCGCCACCCAC 327
QY 241 AACCGTGCCTGCGCTGCGGACCGGCTTCTTCCGACAGCTGCTTCTGCTTGGAGCAC 300
Db 328 AACCGTGCCTGCGCTGCGGACCGGCTTCTTCCGACAGCTGCTTCTGCTTGGAGCAC 387
QY 301 GCATCGTGTCCACCTGCTGCGGCGTGAATGCGCCCGGCGACCCCGAGCCAGAACACGACG 360
Db 388 GCATCGTGTCCACCTGCTGCGGCGTGAATGCGCCCGGCGACCCCGAGCCAGAACACGACG 447
QY 361 TGCAGCGCTGCGCCCGAGGACCTTCTCAGCCAGAGCTCTCAGCTCAGAGCAGTGCACG 420
Db 448 TGCAGCGCTGCGCCCGAGGACCTTCTCAGCCAGAGCTCTCAGCTCAGAGCAGTGCACG 507
QY 421 CCCACCGCACTGCAGCGGCTGCGGCTGCGGCTCAATGTCAGGCTCTTCTCCCAT 480
Db 508 CCCACCGCACTGCAGCGGCTGCGGCTGCGGCTCAATGTCAGGCTCTTCTCCCAT 567
QY 481 GACACCTGTGCAGCTGACCTGCTGCTTCCCTCAGCAGGAGTACAGGAGCTGAG 540
Db 568 GACACCTGTGCAGCTGACCTGCTGCTTCCCTCAGCAGGAGTACAGGAGCTGAG 627
QY 541 GAGTGTAGCGTGCCTGATCGATTTGTGCTTTCAGGACATCTCATCAAGAGCTG 600
Db 628 GAGTGTAGCGTGCCTGATCGATTTGTGCTTTCAGGACATCTCATCAAGAGCTG 687
QY 601 CAGCGCTGTGCAGGCGCTCAGGCGCCCGAGGCGTGGGTCCGACACCAAGGCGCGGC 660
Db 688 CAGCGCTGTGCAGGCGCTCAGGCGCCCGAGGCGTGGGTCCGACACCAAGGCGCGGC 747
QY 661 CGCGCGCTTGCAGCTCAAGCTCGTGGCGCTCAGGAGCTCTTGGGGCGCAGGAC 720
Db 748 CGCGCGCTTGCAGCTCAAGCTCGTGGCGCTCAGGAGCTCTTGGGGCGCAGGAC 807
QY 721 GGGCGCTGTGTGGCGCTGCTGAGCGCTGCGGTGGCGAGATGCCCGGCTGGAG 780
Db 808 GGGCGCTGTGTGGCGCTGCTGAGCGCTGCGGTGGCGAGATGCCCGGCTGGAG 867
QY 781 CGGAGCGTCCGTGAGCGCTTCTCCCTGTGCAC 813
Db 868 CGGAGCGTCCGTGAGCGCTTCTCCCTGTGCAC 900

RESULT 11
AAF62705
ID AAF62705 standard; cDNA; 1055 BP.
XX AC
XX AC
XX AAF62705;
XX
XX
XX 02-MAY-2001 (first entry)
XX Human NTR3 nucleotide sequence.
XX Human; NTR3; tumour necrosis factor receptor; TNF receptor; anti-HIV;
KW antianemic; immunosuppressive; antidiabetic; antiviral; antibacterial;
KW cytosolic; neuroprotective; antiinflammatory; anorectic; vasotropic;
KW antirheumatoid; antiarthritic; cerebroprotective; tuberculostatic;
KW gene therapy; cancer; blood disorder; brain disorder; autoimmune disease;
KW infection; ss.

XX Homo sapiens.
XX OS
XX PN WO200110908-A1.
XX PD 15-FEB-2001.
XX PF 02-AUG-2000; 2000WO-US21287.
XX PR 04-AUG-1999; 99US-0147297.
XX PA (AMGB-) AMGEN INC.
XX PI Hsu H;
XX WPI; 2001-191521/19.
XX P-PSDB; AAB71754.
XX New tumor necrosis factor receptor, NTR3, useful for treating cancers,
PT stroke, anemia, obesity, rheumatoid arthritis and transplantation
PT rejection -
XX
XX Claim 1; Page 128-129; 135pp; English.
XX
CC The present sequence encodes the tumour necrosis factor (TNF) receptor
CC polypeptide NTR3. The NTR3 polynucleotides and polypeptides are useful
CC for treating diseases such as acquired-immunodeficiency syndrome (AIDS),
CC anaemia, autoimmune diseases, cachexia, cancer, cerebral malaria,
CC diabetes mellitus, disseminated intravascular coagulopathy, erythroid
CC sick syndrome, haemorrhagic shock, hepatitis, insulin resistance,
CC leprosy, leukaemia, meningitis, multiple sclerosis, myocardial ischaemia,
CC obesity, rejection of transplanted organs, rheumatoid arthritis, septic
CC shock syndrome, stroke, adult respiratory distress syndrome (ARDS),
CC tuberculosis, and a number of viral diseases. The NTR3 polypeptide is
CC useful for identifying or developing new (ant)agonists of NTR3. It may
CC be used as an immunogen to which antibodies may be raised. NTR3 nucleic
CC acid molecules may be useful as hybridisation probes in diagnostic assays
CC to test, either qualitatively or quantitatively, for the presence of an
CC NTR3 DNA or corresponding RNA in mammalian tissue or bodily fluid
CC samples.
XX
SQ Sequence 1055 BP; 160 A; 369 C; 340 G; 186 T; 0 other;
Query Match 100.0%; Score 813; DB 22; Length 1055;
Best Local Similarity 100.0%; Pred. NO. 5.1e-145;
Matches 813; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTGCGAGAAACACCCACCTTACCCCTGGCGGAGCGAGAGACAGGGAGCGGCTGGTGTGC 60
Db 154 GTGCGAGAAACACCCACCTTACCCCTGGCGGAGCGAGAGACAGGGAGCGGCTGGTGTGC 213
QY 61 GCCCAGTGCCTCCAGAGCAGCTTTGTGAGCGGCGCTGGCGCGAGACAGCCCAACGACG 120
Db 214 GCCCAGTGCCTCCAGAGCAGCTTTGTGAGCGGCGCTGGCGCGAGACAGCCCAACGACG 273
QY 121 TGTGGCGCTGTCCACCGCGCACTACACGAGTTCTGGAACTACCTGGAGCGCTGCCGC 180
Db 274 TGTGGCGCTGTCCACCGCGCACTACACGAGTTCTGGAACTACCTGGAGCGCTGCCGC 333
QY 181 TACTGCAACGCTCTCTGCGGGAGCGTGAAGAGAGGCAAGGGCTTGCAGCGCCACCCAC 240
Db 334 TACTGCAACGCTCTCTGCGGGAGCGTGAAGAGAGGCAAGGGCTTGCAGCGCCACCCAC 393
QY 241 AACCGTGCCTGCGCTGCGGACCGGCTTCTTCCGACAGCTGCTTCTCTTGGAGCAC 300
Db 394 AACCGTGCCTGCGCTGCGGACCGGCTTCTTCCGACAGCTGCTTCTCTTGGAGCAC 453
QY 301 GCATCGTGTCCACCTGCTGCGGCGTGAATGCGCGGCAACCCCGAGAACACGACGACG 360
Db 454 GCATCGTGTCCACCTGCTGCGGCGTGAATGCGCGGCAACCCCGAGAACACGACGACG 513
QY 361 TGCAGCGCTGCGCCCGAGGACCTTCTCAGCCAGAGCTCCTCAGAGCAGTGCAGAGCAGTGCAG 420

QY 541 GAGTGTGAGCGTCCGCTCATCGACTTTGTGGCTTTCAGGACATCTCCATCAGAGGCTG 600
DB 680 GAGTGTGAGCGTCCGCTCATCGACTTTGTGGCTTTCAGGACATCTCCATCAGAGGCTG 739
QY 601 CAGCGCTGTCTGACAGGCGCTTCGAGGCGCCCGAGGCTGGGGTCCGACACCAAGGGCGGGC 660
DB 740 CAGCGCTGTCTGACAGGCGCTTCGAGGCGCCCGAGGCTGGGGTCCGACACCAAGGGCGGGC 799
QY 661 CGCGCGCGCTTGACGTGAAGCTGCGTGGCGGCTCACGGAGTCTCTGGGGGCGCAGGAC 720
DB 800 CGCGCGCGCTTGACGTGAAGCTGCGTGGCGGCTCACGGAGTCTCTGGGGGCGCAGGAC 859
QY 721 GGGGCGCTGTCTGCGGCTGTCTGACAGGCGCTGGCGTGGCGGATGCCGGGCTGGAG 780
DB 860 GGGGCGCTGTCTGCGGCTGTCTGACAGGCGCTGGCGTGGCGGATGCCGGGCTGGAG 919
QY 781 CGGAGCGTCCGTGAGGCGCTTCTCCCTGTGCAC 813
DB 920 CGGAGCGTCCGTGAGGCGCTTCTCCCTGTGCAC 952

RESULT 13
AAV39085
ID AAV39085 standard; cDNA; 1077 BP.
XX
AC AAV39085;
XX
DT 26-OCT-1998 (first entry)
XX
DE Human tumour necrosis factor receptor-6 alpha cDNA.
XX
KW Human tumour necrosis factor receptor-6 alpha; TNFR-6 alpha; TNFR-6 beta;
KW endothelial cells; keratinocytes; normal prostate; apoptosis;
KW prostate tumour tissue; ss.
XX
OS Homo sapiens.
XX
FH Key
FT 25..927
FT CDS
FT /*tag= a
FT /product= "TNFR-6 alpha protein"
FT sig_peptide 25..114
FT /*tag= b
FT mat_peptide 115..924
FT /*tag= c
XX
PN W09830694-A2.
XX
PD 16-JUL-1998.
XX
XX 13-JAN-1998; 98WO-US00153.
XX
PR 14-JAN-1997; 97US-0035496.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Ebner R, Feng P, Gentz RL, Ni J, Ruben SM, Yu G;
XX WPI; 1998-399142/34.
XX P-PSDB; AAW63622.
XX
DR Human tumour necrosis factor receptors 6-alpha and 6-beta - used in
DR the diagnosis of immune system-related disorder(s)
XX
PS Disclosure; Fig 1; 91pp; English.
XX
XX The present sequence represents the human tumour necrosis factor
CC receptor-6 alpha (TNFR-6 alpha) cDNA. The invention also provides
CC for the TNFR-6 beta cDNA (AAV39086). TNFR-6 alpha and TNFR-6 beta are
CC members of the tumour necrosis factor receptor (TNFR) family. TNFRs
CC are expressed in endothelial cells, keratinocytes, normal prostate and
CC prostate tumour tissue. For a number of disorders of these cells,

CC particularly of the immune system, substantially altered (whether
CC increased or decreased) levels of TNFR-6 alpha and/or TNFR-6 beta gene
CC expression can be detected, therefore the TNFR-6 alpha and TNFR-6 beta
CC polypeptides, nucleic acids and antibodies are claimed to be useful in
CC the diagnosis of such disorders. Mutations of the TNFR-6 alpha and
CC TNFR-6 beta genes can also be detected. The TNFR polypeptides are
CC also claimed to be useful for identifying ligands which may be useful
CC in the treatment of apoptosis related disorders.

XX
SQ Sequence 1077 BP; 196 A; 360 C; 326 G; 195 T; 0 other;

Query Match 100.0%; Score 813; DB 19; Length 1077;

Best Local Similarity 100.0%; Pred. No. 5.1e-145;

Matches 813; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGCGAAGAACCCACCTTACCCCTGGCGGACGACAGACAGGAGGCGGTGTGTGC 60

DB 112 GTGGCGAAGAACCCACCTTACCCCTGGCGGACGACAGACAGGAGGCGGTGTGTGC 171

QY 61 GCCCAGTGGCCCCCAGGACCTTTGTGACGGCGCTGGCGGACGACAGCAGCCACGACG 120

DB 172 GCCCAGTGGCCCCCAGGACCTTTGTGACGGCGCTGGCGGACGACAGCAGCCACGACG 231

QY 121 TGTGGCCCGTGTCCACCGCGCCACTACACGCACTTCTGAACTTACCTGGAGCGCTGCCGC 180

DB 232 TGTGGCCCGTGTCCACCGCGCCACTACACGCACTTCTGAACTTACCTGGAGCGCTGCCGC 291

QY 181 TACTGAACGTCCTCTGCGGGAGCGTGAGGAGGACGCGGCTTGCACGCCACCCAC 240

DB 292 TACTGAACGTCCTCTGCGGGAGCGTGAGGAGGACGCGGCTTGCACGCCACCCAC 351

QY 241 AACCGTGCCTGCGGTCGCGCACCGGCTTTTCGCGCAGCGCTTCTGCTTGGAGCAC 300

DB 352 AACCGTGCCTGCGGTCGCGCACCGGCTTTTCGCGCAGCGCTTCTGCTTGGAGCAC 411

QY 301 GCATCGTGTCCACCTGGTGC CGCGCTGATTGCCCGGGCACCCCGCAGCAGAACACGCGAG 360

DB 412 GCATCGTGTCCACCTGGTGC CGCGCTGATTGCCCGGGCACCCCGCAGCAGAACACGCGAG 471

QY 361 TGCAGCGCTGCGCCCCCAGGCACTTCTCAGCAGCAGCTTCCAGCTCAGAGAGTGCAG 420

DB 472 TGCAGCGCTGCGCCCCCAGGCACTTCTCAGCAGCAGCTTCCAGCTCAGAGAGTGCAG 531

QY 421 CCCCACCGCAACTGACGCGCCCTGGGCGCTTCAATGTGCCAGGCTTCTCCCTCCCAT 480

DB 532 CCCCACCGCAACTGACGCGCCCTGGGCGCTTCAATGTGCCAGGCTTCTCCCTCCCAT 591

QY 481 GACACCTGTGCACACGCTGCACTGGCTTCCCGCTCAGCACACGAGGTACCGAGAGCTGAG 540

DB 592 GACACCTGTGCACACGCTGCACTGGCTTCCCGCTCAGCACACGAGGTACCGAGAGCTGAG 651

QY 541 GAGTGTGAGCGTCCGCTCATCGACTTTGTGGCTTTCAGGACATCTCCATCAAGAGCTG 600

DB 652 GAGTGTGAGCGTCCGCTCATCGACTTTGTGGCTTTCAGGACATCTCCATCAAGAGCTG 711

QY 601 CAGCGCTGTGCAGGCGCTTCGAGGCGCCCGGAGGCTGGGGTCCGACACCAAGGGCGGGC 660

DB 712 CAGCGCTGTGCAGGCGCTTCGAGGCGCCCGGAGGCTGGGGTCCGACACCAAGGGCGGGC 771

QY 661 CGCGCGCGCTTGACAGCTGAAGCTGCGTCCGCGGCTCACGAGCTCTGGGGGCGCAGGAC 720

DB 772 CGCGCGCGCTTGACAGCTGAAGCTGCGTCCGCGGCTCACGAGCTCTGGGGGCGCAGGAC 831

QY 721 GGGGCGCTGTGTGCGGCTGTCTGACAGGCGCTGCGGTGCCAGGATGCCCGGGCTGGAG 780

DB 832 GGGGCGCTGTGTGCGGCTGTCTGACAGGCGCTGCGGTGCCAGGATGCCCGGGCTGGAG 891

QY 781 CGGAGCGTCCGTGAGCGCTTCTCCCTGTGCAC 813

DB 892 CGGAGCGTCCGTGAGCGCTTCTCCCTGTGCAC 924

RESULT 14

AAA37772
 ID AAA37772 standard; DNA; 1077 BP.
 XX
 AC AAA37772;
 XX
 DT 04-DEC-2000 (first entry)
 XX
 DE Human tumour necrosis factor receptor-6 alpha coding sequence.
 XX
 KW Human; Tumour necrosis factor receptor 6; TNFR-6alpha; TNFR-6beta;
 KW ocular neovascularisation; solid tumour; malignancy; prostate cancer;
 KW breast cancer; colon cancer; diabetic retinopathy; microbial infection;
 KW pre-maturity macular degeneration; allergy; inflammation; tissue damage;
 KW thyroid associated ophthalmopathy; cell damage; parasitic infection;
 KW bone disease; osteoporosis; atherosclerosis; cardiovascular disease;
 KW neurodegenerative disorder; Alzheimer's disease; immune disorder;
 KW graft rejection; rheumatism; liver disease; autoimmune diabetes; asthma;
 KW psoriasis; septic shock; ulcerative colitis; therapy; ds.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 25..927
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 FT /product= TNFR-6alpha
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 PD 08-SEP-2000.
 XX
 PF 03-MAR-2000; 2000MO-US05686.
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 PR 04-MAR-1999; 99US-0121774.
 PR 12-MAR-1999; 99US-0124092.
 PR 27-APR-1999; 99US-0131279.
 PR 30-APR-1999; 99US-0131964.
 PR 02-AUG-1999; 99US-0146371.
 PR 01-DEC-1999; 99US-0168235.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Gentz RL, Ni J, Ebner R, Yu G, Ruben SM, Feng P;
 XX
 DR WPI: 2000-572174/53.
 DR P-PSDB; AAY90357.
 XX
 PT Nucleic acids encoding human tumour necrosis factor receptor (TNFR)
 PT PT Alzheimer's disease, osteoporosis and graft rejection -
 XX
 PS Claim 2, Fig 1, 332pp; English.
 XX
 CC This sequence encodes the human tumour necrosis factor receptor 6
 CC alpha (TNFR-6alpha) of the invention. The TNFR-6alpha and TNFR-6beta DNA
 CC and protein sequences can be used in the prevention, treatment and
 CC diagnosis of diseases associated with inappropriate TNFR expression. The
 CC nucleic acids, polypeptides, antibodies, agonists and antagonists against
 CC these may be used for the treatment of a range of conditions such as
 CC disorders associated with neovascularisation (especially ocular
 CC neovascularisation) (such as solid tumours and malignancies (e.g.
 CC prostate cancer, breast cancer and colon cancer), diabetic retinopathy
 CC and pre-maturity macular degeneration), allergies, inflammation,
 CC thyroid associated ophthalmopathy (tissue/cell damage, wounds, microbial
 CC and parasitic infections, bone disease (e.g. osteoporosis),
 CC atherosclerosis, pain, cardiovascular disease (e.g. stroke),
 CC neurodegenerative disorders (e.g. Alzheimer's disease), immune
 CC disorders (e.g. graft rejection), rheumatism, liver disease,
 CC autoimmune diabetes, asthma, psoriasis, septic shock and ulcerative
 CC colitis.
 CC
 SQ Sequence 1077 BP; 196 A; 360 C; 326 G; 195 T; 0 other;
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 Query Match 100.0%; Score 813; DB 21; Length 1077;

Best Local Similarity 100.0%; Pred. No. 5.1e-145;
 Matches 813; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 DB 112 GTGGCAAAAACACCCACTAACCCCTGGCGGAGACAGAGAGAGAGGAGGGCTGGTGC 171
 QY 61 GCCAGTGGCCCCCAGAGCACTTTGTGACAGCGCGTGCCTGCCGAGACAGCCCCAGACG 120
 DB 172 GCCAGTGGCCCCCAGAGCACTTTGTGACAGCGCGTGCCTGCCGAGACAGCCCCAGACG 231
 QY 121 TGTGGCCCGTGTCCACCGCGCCACTACAGCAGTTTGGAACTACCTGGAGCCCTGCCG 180
 DB 232 TGTGGCCCGTGTCCACCGCGCCACTACAGCAGTTTGGAACTACCTGGAGCCCTGCCG 291
 QY 181 TACTGCAACGCTCTCTGCGGGGAGCGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
 DB 292 TACTGCAACGCTCTCTGCGGGGAGCGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 351
 QY 241 AACCGTGCCTGCGCGTGCAGCAGCGGCTTCTTGCAGCAGCGTGTCTTGTGAGACAG 300
 DB 352 AACCGTGCCTGCGCGTGCAGCAGCGGCTTCTTGCAGCAGCGTGTCTTGTGAGACAG 411
 QY 301 GCATGCTGTCCACCTGATGCGGCGGTGATTTGCCCGGAGACCCCAAGCAGACAGCAG 360
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 QY 361 TGGCAGCCGTCGCCCCCAGGACACTTCTCAGCCAGCAGACTCCAGCTCAGAGAGTGCAG 420
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 DB 592 GACACCTGTGCAACAGCTGCACTGCTTCCCTCAGACCAAGGATCCAGAGAGCTGAG 651
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 DB 892 CGGAGCGTCCGTGAGGCGCTTCTCCCTGAGCAG 924
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 ID AAD33281 standard; cDNA; 1077 BP.
 XX
 AC AAD33281;
 XX
 DT 01-JUL-2002 (first entry)
 XX
 DE Human tumour necrosis factor receptor (TNFR)-6alpha cDNA.
 XX
 KW Human; tumour necrosis factor receptor; TNFR-6alpha; TNFR-6beta; therapy;
 KW immune system-related disorder; inflammatory disease; immunosuppressive;
 KW bowel disease; encephalitis; atherosclerosis; gastrointestinal-Gen;

KW autoimmune disease; systemic lupus erythematosus; rheumatoid arthritis;
KW multiple sclerosis; Crohn's disease; autoimmune encephalitis; allergy;
KW graft versus host disease; GVHD; antiinflammatory; psoriasis; arthritis;
KW neuroprotective; antiarteriosclerotic; dermatological; asthma; receptor;
XX gene; ss.
OS Homo sapiens.

XX Key Location/Qualifiers
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FT mat_peptide 115..924
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PN WO200218622-A2.

XX 07-MAR-2002.

XX 24-AUG-2001; 2001WO-US26396.

XX 25-AUG-2000; 2000US-227598P.

PR 21-NOV-2000; 2000US-252131P.

PR 06-JUL-2001; 2001US-303224P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Gentz RL, Ebner R, Yu G, Ruben SM, Ni J, Peng P;

XX WPI; 2002-281068/32.

XX P-PSDB; AAE20848.

XX Novel nucleic acid molecules comprising a polynucleotide encoding human
PT tumor necrosis factor receptor (TNFR)-6alpha and 6beta polypeptides
PT useful for treating disease e.g. inflammatory and autoimmune disorders
PT -
XX

PS Example 1; Fig 1; 350pp; English.

XX The invention relates to human tumour necrosis factor receptor (TNFR)-
CC galpha and 6beta protein and their corresponding nucleic acids. The
CC invention provides screening methods for identifying agonists and
CC antagonists of TNFR-6alpha and 6beta activity. The invention also
CC provides diagnostic and therapeutic methods for detecting and treating
CC immune system-related disorders. The method is useful for treating or
CC preventing an inflammatory disease or disorder selected from bowel
CC disease, encephalitis, atherosclerosis and psoriasis, an autoimmune
CC disease or disorder selected from systemic lupus erythematosus,
CC arthritis, rheumatoid arthritis, multiple sclerosis, Crohn's disease,
CC and autoimmune encephalitis, graft versus host disease (GVHD), and an
CC allergy or asthma. The present sequence is human TNFR-6alpha cDNA.

SQ Sequence 1077 BP; 196 A; 360 C; 326 G; 195 T; 0 other;

Query Match 100.0%; Score 813; DB 24; Length 1077;
Best Local Similarity 100.0%; Pred. No. 5,1e-145;
Matches 813; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGCAGAAAACACCCACTACCCCTGGCGGAGCAGACAGAGGAGCGGCTGGTGTC 60
DB 112 GTGGCAGAAAACACCCACTACCCCTGGCGGAGCAGACAGAGGAGCGGCTGGTGTC 171
QY 61 GCCCAGTGCCCCCAGGACCTTTGTGACGGCGGTGCCGAGACACCCACGACG 120
DB 172 GCCCAGTGCCCCCAGGACCTTTGTGACGGCGGTGCCGAGACACCCACGACG 231
QY 121 TGTGGCCCGTGTCCACCGCCCACTACACGAGTTCTGGAACTACCTGGAGCGCTGCCG 180
DB 232 TGTGGCCCGTGTCCACCGCCCACTACACGAGTTCTGGAACTACCTGGAGCGCTGCCG 291

QY 181 TACTGCAACGTCCTCTGCGGAGCGTGAGGAGGAGCGGCTTGCCACGCCACCCAC 240
DB 292 TACTGCAACGTCCTCTGCGGAGCGTGAGGAGGAGCGGCTTGCCACGCCACCCAC 351
QY 241 AACCGTGCCTGCGGCTGCCGACCCGCTTCTTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 300
DB 352 AACCGTGCCTGCGGCTGCCGACCCGCTTCTTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 411
QY 301 GCATCGTGTCCACGCTGGTGCCTGCGGCTGATGCCCCGGGACCCCCAGCAGAACACGACG 360
DB 412 GCATCGTGTCCACGCTGGTGCCTGCGGCTGATGCCCCGGGACCCCCAGCAGAACACGACG 471
QY 361 TGCAGCGCTGCCCGCCCGGACGCTTCTCAGCCAGCAGCTCCAGCTCAGCAGAGTCCGACG 420
DB 472 TGCAGCGCTGCCCGCCCGGACGCTTCTCAGCCAGCAGCTCCAGCTCAGCAGAGTCCGACG 531
QY 421 CCCCACCGCAACTGTCACGCGCCCTGGGCTTTCCTCAATGTGCCAGGCTCTTCTCTCCCAT 480
DB 532 CCCCACCGCAACTGTCACGCGCCCTGGGCTTTCCTCAATGTGCCAGGCTCTTCTCTCCCAT 591
QY 481 GACACCTGTGACACGAGCTGCTGCTTCCCGCTCAGCACGAGGTACAGGAGCTGAG 540
DB 592 GACACCTGTGACACGAGCTGCTGCTTCCCGCTCAGCACGAGGTACAGGAGCTGAG 651
QY 541 GAGTGTGAGCGTGCGCTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG 600
DB 652 GAGTGTGAGCGTGCGCTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG 711
QY 601 CAGCGGCTGCTGCAGGCGCTCGAGGCCCCGAGGGCTGGGGTCCGACACCAAGGGCGGGC 660
DB 712 CAGCGGCTGCTGCAGGCGCTCGAGGCCCCGAGGGCTGGGGTCCGACACCAAGGGCGGGC 771
QY 661 CCGCGGCGCTTGCAGCTGAAGCTGCGTGGCGGCTTCA CGGAGCTCTCTGGGGGCGCAGGAC 720
DB 772 CCGCGGCGCTTGCAGCTGAAGCTGCGTGGCGGCTTCA CGGAGCTCTCTGGGGGCGCAGGAC 831
QY 721 GGGGCGCTGCTGGTGGCGGCTGCTGAGGCGCTGCGGCTGGCCAGGATGCCCGGCTGGAG 780
DB 832 GGGGCGCTGCTGGTGGCGGCTGCTGAGGCGCTGCGGCTGGCCAGGATGCCCGGCTGGAG 891
QY 781 CGGAGCGCTCCGTGAGCGCTTCTCTCCCTGTGCAC 813
DB 892 CGGAGCGCTCCGTGAGCGCTTCTCTCCCTGTGCAC 924

Search completed: January 6, 2003, 13:55:32
Job time : 233 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: January 6, 2003, 13:45:41 ; Search time 1966 Seconds
(without alignments)
6697.320 Million cell updates/sec

Title: US-09-936-024-2

Perfect score: 813

Sequence: 1 gtcgcagaacaccacaccta.....agcccttcctccctcgtgcac 813

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

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1: em_estda.*
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3: em_estln.*
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9: gb_est1.*
10: gb_est2.*
11: gb_hic.*
12: gb_est3.*
13: gb_est4.*
14: gb_est5.*
15: em_estfun.*
16: em_estom.*
17: gb_gss.*
18: em_gss_hum.*
19: em_gss_inv.*
20: em_gss_pla.*
21: em_gss_vrt.*
22: em_gss_fun.*
23: em_gss_mam.*
24: em_gss_mus.*
25: em_gss_other.*
26: em_gss_pro.*
27: em_gss_rod.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	577	70.6	679	BE878006 601489784
5	573.8	863	14	BQ687526 AGENCOURT
6	567.2	572	14	BM767535 K-EST0050

7	541.8	66.6	1203	13	BM480312	BM480312 AGENCOURT
8	529	65.1	1037	12	BG679499	BG679499 602627514
9	499.8	61.5	874	12	BF339551	BF339551 602039016
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16	405	49.8	606	14	BM767446	BM767446 K-EST0049
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18	400.2	49.2	605	14	BM767418	BM767418 K-EST0049
19	393.8	48.4	616	14	BM743072	BM743072 K-EST0016
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24	387	47.6	588	14	BM756087	BM756087 K-EST0034
25	387	47.6	593	14	BM759026	BM759026 K-EST0038
26	383.8	47.2	486	14	BM831338	BM831338 K-EST0105
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35	315.2	38.8	524	14	BM833454	BM833454 K-EST0108
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ALIGNMENTS

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DEFINITION 603035863F1 NIH_MGC_115 Homo sapiens CDNA clone IMAGE:5176910 5',
mRNA sequence.
ACCESSION BI821789
VERSION BI821789.1 GI:15933339
KEYWORDS EST.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 1118)
NIN-MGC <http://mgc.nci.nih.gov/>.
AUTHORS NIH-MGC
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LHAM11440 row: n column: 15
High quality sequence stop: 758.
Location/Qualifiers
1. 1118

FEATURES
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male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
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RESULT 2
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DEFINITION 601492609F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3894794 5',
mRNA sequence.
ACCESSION BE878908
VERSION BE878908.1 GI:10327684
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 617)
NIH-MGC http://mgs.nci.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTF/Gazdar
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLaM9685 row: a column: 03
High quality sequence stop: 617.
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/tissue_type="large cell carcinoma, undifferentiated"
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/note="Organ: lung; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.1 kb. Library constructed by Life
Technologies."
BASE COUNT 91 a 224 c 203 g 99 t
ORIGIN
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QY 216 GGCACGGGCTTGCCACGCCACCAACCGTGCCTGCCGTGCTGCCGACCGGCTTCTTCCG 275
Db 63 GGCACGGGCTTGCCACGCCACCAACCGTGCCTGCCGTGCTGCCGACCGGCTTCTTCCG 122
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Qy      636  CTGGGGTCCGACACCAAGGGCGGGCGCGGCTTGCAGCTGAAGTGGGTGGGGCT 695
Db      483  CTGGGGTCCGACACCAAGGGCGGGCGCGGCTTGCAGCTGAAGTGGGTGGGGCT 542
Qy      696  CACGAGCTCTCTGGGGCGGAGACGAGGCGGCTGCTGTGTGCGCTGTGAGGCGCTGCG 755
Db      543  CACGAGCTCTCTGGGGCGGAGACGAGGCGGCTGCTGTGTGCGG-TGCTGACAGGCGCTGCG 601
Qy      756  CGTGGC 761
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RESULT 3
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VERSION     BM680786.1 GI:18990682
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SOURCE      human.
ORGANISM   Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 728)
AUTHORS    Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE      Normalization and subtraction: two approaches to facilitate gene
            discovery
JOURNAL    Genome Res. 6 (9), 791-806 (1996)
MEDLINE    97044477
COMMENT     Contact: Soares, MB
            Program for Rat Gene Discovery and Mapping
            University of Iowa
            451 Eckstein Medical Research Building Iowa City, IA 52242, USA
            Tel: 319 335 8250
            Fax: 319 335 9565
            Email: msoares@blue.weeg.uiowa.edu
            Tissue Procurement: Dr. Gregg Hageman
            cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
            DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
            Clone Distribution: Researchers may obtain clones from Research
            Genetics (www.resgen.com).
            Seq primer: M13 Forward
            POLYA=Yes.

FEATURES
source      location/Qualifiers
            1..728
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /clone="UI-E-BO1-a3c-j-12-0-UI"
            /clone_1ib="UI-E-BO1"
            /tissue_type="fetal eye"
            /dev_stage="fetal"
            /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
            /note="Organ: eye; Vector: pT73-Pac (Pharmacia) with a
            modified polylinker; Site 1: EcoR I; Site 2: Not I;
            UI-E-BO1 is a normalized cDNA library containing the
            following tissue(s): fetal eye. The library was
            constructed according to Bonaldo, Lennon and Soares,
            Genome Research, 6:791-806, 1996. First strand cDNA
            synthesis was primed with an oligo-dT primer containing a
            Not I site. Double stranded cDNA was ligated to an EcoR I
            adaptor, digested with Not I, and cloned directionally
            into pT73-Pac vector. The oligonucleotide used to prime
            the synthesis of first-strand cDNA contains a library tag
            sequence that is located between the Not I site and the
            (dT)18 tail. The sequence tag for this library is
            CCGGTATACC. This library was created for the program, Gene
            Discovery in the Visual System, supported by National Eye

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BASE COUNT  133 a 218 c 248 g 129 t
ORIGIN
Institute (NEI).
TAG LIB=UI-E-BO1
TAG TISSUE=human fetal eye
TAG_SBO=CGCGTATACC"
Query Match      71.0%; Score 577.4; DB 14; Length 728;
Best Local Similarity 99.3%; Pred. No. 1,7e-98;
Matches 591; Conservative 0; Mismatches 1; Indels 3; Gaps 1;

Qy      222  GGCCTGCGACGCCACCCACAACTGCTGCGCTGCGCTGCGACCGGCTTCTTGCGGACGC 281
Db      705  GGCCTGCGACGCCACCCACAACTGCTGCGCTGCGCTGCGACCGGCTTCTTGCGGACGC 646
Qy      282  TGGTTTCTGCTTGGAGACGACATCGTGTCCAACTGATGCGGGGTATGCCCCGGGAC 341
Db      645  TGGTTTCTGCTTGGAGACGACATCGTGTCCAACTGATGCGGGGTATGCCCCGGGAC 586
Qy      342  CCCAGCAGAAACAGCCAGTGCAGGCGTGCCTCCCGGACGACCTTCTCAGCCAGAGCTC 401
Db      585  CCCAGCAGAAACAGCCAGTGCAGGCGTGCCTCCCGGACGACCTTCTCAGCCAGAGCTC 526
Qy      402  CAGCTCAGAGCAGTGCAGGCCCGCAACTGACGAGCCCTGAGCCCTCAATGT 461
Db      525  CAGCTCAGAGCAGTGCAGGCCCGCAACTGACGAGCCCTGAGCCCTCAATGT 466
Qy      462  GCCAGGCTCTTCTCTCCATATACACCTGTGTACACAGTGTGCTTCCCTCAGAC 521
Db      465  GCCAGGCTCTTCTCTCCATATACACCTGTGTACACAGTGTGCTTCCCTCAGAC 406
Qy      522  CAGGATAC--CAGGAGCTGAGAGTGTGAGCGTGCCTGATGACTTGTGCTTTCCA 578
Db      405  CAGGATACAGAGCAGAGCTGAGAGTGTGAGCGTGCCTGATGACTTGTGCTTTCCA 346
Qy      579  GGAATCTTCATCAAGAGGCTGAGCGGCTGTGACAGCCCTTGAGGCCCGGAGGGCTG 638
Db      345  GGAATCTTCATCAAGAGGCTGAGCGGCTGTGACAGCCCTTGAGGCCCGGAGGGCTG 286
Qy      639  GGGTCCGACACCAAGGGCGGGCGGCGGCTTGCAGCTGAAGCTGTGCGGCTCAC 698
Db      285  GGGTCCGACACCAAGGGCGGGCGGCGGCTTGCAGCTGAAGCTGTGCGGCTCAC 226
Qy      699  GGAATCTCTGGGGGCGAGGACGGGGCGCTGATGAGCGCTCTCAGAGCGTGGCGGT 758
Db      225  GGAATCTCTGGGGGCGAGGACGGGGCGCTGATGAGCGCTCTCAGAGCGTGGCGGT 166
Qy      759  GGCCAGGATCCCGGGCTGAGCGAGCGTCCGTGAGCGCTTCTCTCTGTGCAC 813
Db      165  GGCCAGGATCCCGGGCTGAGCGAGCGTCCGTGAGCGCTTCTCTCTGTGCAC 111

RESULT 4
BE878006 679 bp mRNA linear EST 20-OCT-2000
LOCUS      BE878006
DEFINITION 601489784F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3891908 5',
            mRNA sequence.
ACCESSION  BE878006
VERSION     BE878006.1 GI:10326782
KEYWORDS   EST.
SOURCE      human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 679)
AUTHORS    NIH-MGC http://mgc.nci.nih.gov/.
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL    Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgabbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTF/Gazdar
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

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DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM9677 row: h column: 21
High quality sequence stop: 672.
Location/Qualifiers
1. .679
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="IMAGE:3891908"
/clone_lib="NIH_MGC_69"
/tissue_type="large cell carcinoma, undifferentiated"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lung; Vector: pCMV-SPORT6; Site: 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dr. Average insert size 1.1 kb. Library constructed by Life Technologies."

BASE COUNT 113 a 239 c 204 g 123 t
ORIGIN

Query Match 71.0%; Score 577; DB 12; Length 679;
Best Local Similarity 100.0%; Pred. No. 1.9e-98;
Matches 577; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 237 CCACAAACGTCCTGCGCTGCGCAGCAGGCTTCTTCGCGCAGCGCTGCTGCTTGA 296
Db 11 CCACAAACGTCCTGCGCTGCGCAGCAGGCTTCTTCGCGCAGCGCTGCTTGA 70
QY 297 GCAGCATGTCCTACCTGTCGCGGCTGATTCGCCCGGACCCCGCAGCAGACAC 356
Db 71 GCAGCATGTCCTACCTGTCGCGGCTGATTCGCCCGGACCCCGCAGCAGACAC 130
QY 357 GCAGTGCAGCGCTGCCCCCGCAGCAGCTTCTCAGCAGCAGCTCCAGCTCAGCAGTG 416
Db 131 GCAGTGCAGCGCTGCCCCCGCAGCAGCTTCTCAGCAGCAGCTCCAGCTCAGCAGTG 190
QY 417 CCAGCCCGCAGCACTGACGCGGCTTGGGCTGCGGCTCAATGTGCGAGGCTTCTCTC 476
Db 191 CCAGCCCGCAGCACTGACGCGGCTTGGGCTGCGGCTCAATGTGCGAGGCTTCTCTC 250
QY 477 CCATGACACCTGTGACGAGCTGACCTGCTTCCCTCAGCAGCAGGCTACAGAGC 536
Db 251 CCATGACACCTGTGACGAGCTGACCTGCTTCCCTCAGCAGCAGGCTACAGAGC 310
QY 537 TGAGGAGTGTGAGCGTCCGCTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAG 596
Db 311 TGAGGAGTGTGAGCGTCCGCTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAG 370
QY 597 GCTGACGCGCTGTGAGGCTTCGAGGCTTCGAGGCTTCGAGGCTTCGAGGCTTCGAGGCT 656
Db 371 GCTGACGCGCTGTGAGGCTTCGAGGCTTCGAGGCTTCGAGGCTTCGAGGCTTCGAGGCT 430
QY 657 GGGCGCGCGGCTTGCAGCTGAGCTGCGTCCGCGCTCAGCGAGCTCCTGGGGCGCA 716
Db 431 GGGCGCGCGGCTTGCAGCTGAGCTGCGTCCGCGCTCAGCGAGCTCCTGGGGCGCA 490
QY 717 GGACGGGGCTGTGCTGGGCTGTGCTGAGGCTGCTGCGGCTGCGCAGGATGCGCGGCT 776
Db 491 GGACGGGGCTGTGCTGGGCTGTGCTGAGGCTGCTGAGGCTGCGGCTGCGCAGGATGCGCGGCT 550
QY 777 GGACGGAGCGTGTGAGGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 813
Db 551 GGACGGAGCGTGTGAGGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 587

RESULT 5
BQ687526
LOCUS BQ687526 863 bp mRNA linear EST 15-JUL-2002
DEFINITION AGENCOURT_8345883 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6250691
5', mRNA sequence.
ACCESSION BQ687526
VERSION BQ687526.1 GI:21812842

KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 863)
NIH-MGC http://mgc.nci.nih.gov/
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM2394 row: c column: 12
High quality sequence stop: 599.
Location/Qualifiers
1. .863
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="IMAGE:6250691"
/clone_lib="NIH_MGC_110"
/tissue_type="ductal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: pancreas; Vector: pOTB7; Site: 1: XhoI; Site 2: EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
Note: this is a NIH_MGC Library."

BASE COUNT 133 a 312 c 276 g 141 t
ORIGIN

Query Match 70.6%; Score 573.8; DB 14; Length 863;
Best Local Similarity 94.8%; Pred. No. 8e-98;
Matches 637; Conservative 0; Mismatches 28; Indels 7; Gaps 4;
QY 1 GTGGCAGAAACACCCACCTTACCCCTGGCGGACGACAGACAGGAGCGGCTGGTGTGC 60
Db 149 GTGGCAGAAACACCCACCTTACCCCTGGCGGACGACAGACAGGAGCGGCTGGTGTGT 208
QY 61 GCCCAGTGGCCCCCAGGACCTTTGTGACGCGGCTGCGCGGACAGACAGCCCGCAGACG 120
Db 209 GCCCAGTGGCCCCCAGGACCTTTGTGACGCGGCTGCGCGGACAGACAGCCCGCAGACG 268
QY 121 TGTGGCCCGTGTCCACCGCGCCACTACAGCAGTTCTGGAACTTACCTGGAGCGCTGCGC 180
Db 269 TGTGGCCCGTGTCCACCGCGCCACTACAGCAGTTCTGGAACTTACCTGGAGCGCTGCGC 328
QY 181 TACTGCAACGTCCTCTGCGGGAGCGCTGAGGAGGACAGCGGCTTGCACCGCCACCCCAC 240
Db 329 TACTGCAACGTCCTCTGCGGGAGCGCTGAGGAGGACAGCGGCTTGCACCGCCACCCCAC 388
QY 241 AACCGTGCCTGCGCTGCGCAGCCGCTTCTTCGCGCAGCTGGTTCCTTGGAGCAC 300
Db 389 AACCGTGCCTGCGCTGCGCAGCCGCTTCTTCGCGCAGCTGGTTCCTTGGAGCAC 448
QY 301 GCATCGTGTCCACCTGCTGCGCGCTGATTGCCCCGGGACCCCGCAGCAGCAACACGACG 360
Db 449 GCATCGTGTCCACCTGCTGCGCGCTGATTGCCCCGGGACCCCGCAGCAGCAACACGACG 508
QY 361 TGCCAGCGGTGCCCGCCAGGACCTTCTCAGCCAGCAGCTTCCAGCTCAGAGCAGTGCCAG 420
Db 509 TGCCAGCGGTGCCCGCCAGGACCTTCTCAGCCAGCAGCTTCCAGCTCAGAGCAGTGCCAG 568
QY 421 CCCCAGCGCACTGCACGG--CCCTGGGCTTGGCCCTCATGTGCCAGGCTCTTCTCTCC 478

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Db 569 CCCACCGCACTGACAGGCGCCCTGGGCGCTCAATGTCAGAGCTCTTCTCCC 628
Qy 479 ATGACACCCCTGTGCACAGCTGCACTGGCTTCCCTCCAGACACGAGGTACCAAGA--GC 536
Db 629 ATACACGCTGTGCACAGCTGCACTGGCTTCCCTCCAGACACGAGGTACCAAGAAGCT 688
Qy 537 TGAGAGTGTGACGCTGCGCTCATCGAC-TTGTGCTTTCCAGACATCTCATCAAGA 595
Db 689 GAGGAAGTGTGACGCTGCGCTCATCGACCTTTGTGCTTTCCAGACATCTCATCAAGA 748
Qy 596 GGTGAGCGGCTGTGCAGAGCCCTGAGGCCCCGGA--GGGCTGGGTCCGACACCAAG 653
Db 749 AGTGTGAGCGGCTGTGCAGAGCCCTGAGGCCCCGGAAGGCTGGGGGTCCGAACCA 808
Qy 654 GCGGCGCGCGC 665
Db 809 GGGCGGGCGCGC 820

RESULT 6
LOCUS BM767535 572 bp mRNA linear EST 04-MAR-2002
DEFINITION K-EST0050015 S1SNUS52 Homo sapiens cDNA clone S1SNUS52-3-B03 5',
ACCESSION BM767535
VERSION BM767535.1 GI:19097150
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.
1 (bases 1 to 572)
Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
21C Frontier Korean EST Project 2001
Unpublished (2002)
Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 3 row: E column: 03
High quality sequence stop: 572.
Location/Qualifiers
1..572
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="S1SNUS52-3-E03"
/clone_1ib="S1SNUS52"
/sex="F"
/tissue_type="Ascites"
/cell_type="Lymphoblast-like"
/lab_host="Top10F"
/notes="Organ: Stomach; Vector: pCNS; Site: 1: EcoRI;
Site_2: NotI; The poly (A) + RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then deapped
with tabacco acid pyrophosphatase (TAP). The deapped
intact mRNA was ligated of T4 RNA ligase and the first strand
cDNA was synthesized from oligo dT-selected mRNA by
priming with dt-tailed vector. The dt-tailed vector was
adjusted to have about 60nt. The cDNA vector was
circularized with E. coli DNA ligase after digestion of
EcoRI which site is also included in vector. An RNA strand
converted to a DNA strand by Okayama-Berg method. The
obtained cDNA vectors were used for transformation of
competent cells E. coli Top10F by electroporation method.
The cDNA libraries constructed by this method are
full-length enriched cDNA library. After analyzing and

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sequencing about 2,000 ~ 3,000 colonies in original cDNA
library, the abundant cDNAs were selected and amplified by
PCR reaction using vector region primer including T7
promotor as 5' primer and Nidrl14 as 3' primer. The PCR
products were used as template for synthesis of
biotinylated single stranded RNA by in vitro transcription
reaction. The synthesized RNA probes were hybridized with
antiesense single stranded cDNA prepared from original
library and incubated with avidin-gel. After removing
DNA-RNA hybrids by centrifuge, the subtracted cDNA
libraries were constructed by transformation of the
remaining DNA into competent cells E. coli Top10F with
electroporation method."

BASE COUNT      90 a      213 c      174 g      95 t
ORIGIN

Query Match      69.8%; Score 567.2; DB 14; Length 572;
Best Local Similarity 99.5%; Pred. No. 1.3e-96;
Matches 569; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 117 GACGTGTGGCCCGTGTCCACCGGCGCACTACAGCACTTCTGGAATCACTGAGGCGTG 176
Db 1 GACGTGTGGCCCGTGTCCACCGGCGCACTACAGCACTTCTGGAATCACTGAGGCGTG 60
Qy 177 CCGCTACTGCAACGTCCTCTGCGGGAGCGGTGAGAGAGCAAGGCGCTTGCCACGCCAC 236
Db 61 CCGCTACTGCAACGTCCTCTGCGGGAGCGGTGAGAGAGCAAGGCGCTTGCCACGCCAC 120
Qy 237 CCACAAACGTCCTCTGCGGTGCGGACCGGCTTTCTTGCGGACAGCTGTGTTCTTGGA 296
Db 121 CCACAAACGTCCTCTGCGGTGCGGACCGGCTTTCTTGCGGACAGCTGTGTTCTTGGA 180
Qy 297 GCAAGCATGTGTGTCACCTGTGTGCGGGCGGTGATGCGCGGGGACCCCGACAGAAC 356
Db 181 GCAAGCATGTGTGTCACCTGTGTGCGGGCGGTGATGCGCGGGGACCCCGACAGAAC 240
Qy 357 GCAGTGCACAGCGGTGCGGCGGCGGACGCTTCTCAGCCAGCACTCAGCTCAGAGAGTG 416
Db 241 GCAGTGCACAGCGGTGCGGCGGCGGACGCTTCTCAGCCAGCACTCAGCTCAGAGAGTG 300
Qy 417 CCAGCCCAACCGCAACTGCAAGCGGCGGCTGTGCGCTCAATGTGTCAGGCTTTCTTC 476
Db 301 CCAGCCCAACCGCAACTGCAAGCGGCGGCTGTGCGCTCAATGTGTCAGGCTTTCTTC 360
Qy 477 CCATGACACCGCTGTGACACGCTGCACTGCTTCCCTCAGACACGAGGTACAGAGAG 536
Db 361 CCATGACACCGCTGTGACACGCTGCACTGCTTCCCTCAGACACGAGGTACAGAGAG 420
Qy 537 TGAGAGTGTGAGCGTGCAGCGCTCATCGACTTTGTGCTTCCAGACATCTCATCAAGAG 596
Db 421 TGAGAGTGTGAGCGTGCAGCGCTCATCGACTTTGTGCTTCCAGACATCTCATCAAGAG 480
Qy 597 GCTGACGCGGCTGTGACAGCGCTTCAGAGCCCGGAGAGGCTGGGGTCCGACCAAGGCG 656
Db 481 GCTGACGCGGCTGTGACAGCGCTTCAGAGCCCGGAGAGGCTGGGGTCCGACCAAGGCG 540
Qy 657 GGGCGCGCGGCGCTTGCACTGAAGTGCCTC 688
Db 541 GGGCGCGCGGCGCTTGCACTGAAGTGCCTC 572

RESULT 7
LOCUS BM480312 1203 bp mRNA linear EST 05-FEB-2002
DEFINITION AGENCOURT_6424187 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:5491790
ACCESSION BM480312
VERSION BM480312.1 GI:18529354
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.

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QY 301 GCATGTCCTCACCCTGTCGCGGCGGTGATTTGCCCCGGAGCACCCCGACAGACAGCAG 360
Db 494 GCATGTCCTCACCCTGTCGCGGCGGTGATTTGCCCCGGAGCACCCCGACAGACAGCAG 553
QY 361 TGCACGCGTGTGCCCCCGAGGACCTTCTCAGCCAGCAGCTTCACTAGAGCAATGCGCAG 420
Db 554 TGCACGCGTGTGCCCCCGAGGACCTTCTCAGCCAGCAGCTTCACTAGAGCAATGCGCAG 613
QY 421 CCCCACGCGCACTGACGCGGCTGAGGCTGGGCTCCTCATGTCAGGAGCTTCTTCCCAT 480
Db 614 CCCCACGCGCACTGACGCGGCTGAGGCTGGGCTCCTCATGTCAGGAGCTTCTTCCCAT 672
QY 481 GACACCTGTG-TGACACAGCTGAC-TGACTTCCCTCAGACACAGGATACAGAGACTG 538
Db 673 GACACCTGTGTGACAGCTGACCTTGGCTTCCCTCAGACACAGGATACAGAGACTG 732
QY 539 AGGAGTGTG-AGCTGCTGCT-CATGACTTGTGGCTTTC-----AGGACATCTCC 588
Db 733 AGGAGTGTGAGGCTGCTGCTCATGACTTGTGGCTTTC-----AGGACATCTCATC 792
QY 589 ATCAAGAGCTGACGCGGCTGCTGACGCGCT---CGAGGCGCGAGAGGCTGGGCTCCG 645
Db 793 AAGAGAGCTTGTGACGCGGCTGCTGACGCGCTTCCAGAGGCGCGAGGCTGGGCTCCG 852
QY 646 ACAACAGAGGCGGCGCGCGGCTTGTGACGCTGCTGCGCGGCTTCAAGAGCTC 705
Db 853 ACAACAGAGGCGGCGCGCGGCTTGTGACGCTTGAAGCTTGGCTGGGCGGCTTCAAGAGG 912
QY 706 CTGGGGGCGCAGACGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 765
Db 913 TCCGGGGGCGCGCAGAGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 970
QY 766 ATGCGCGGCTGAGAGGCGGAGCTGCTGAGAGCTTCTCTCCCTG 808
Db 971 -ATGCGCGCTGAGAGGCGGAGCGCGAGCGCTTCTCTCCGCTG 1011

RESULT 9

BF339551

LOCUS BF339551 874 bp mRNA linear EST 22-NOV-2000
DEFINITION 602039016F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:418695
5', mRNA sequence.

ACCESSION

BF339551

BF339551.1 GI:11286006

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Homo sapiens
human.
Mammalia; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 874)
NIH-MGC http://mgc.ncl.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: David N. Louis, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: LHAM508 row: p column: 04
High quality sequence stop: 701.
Location/Qualifiers

FEATURES

source

1. 874
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:418695"
/clone_lib="NCI_CGAP_Brn64"
/tissue_type="glioblastoma with EGFR amplification"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NCI;

Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.57 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

Query Match 61.5%; Score 499.8; DB 12; Length 874;

Best Local Similarity 87.8%; Pred. No. 5.7e-84;

Matches 568; Conservative 0; Mismatches 77; Indels 2; Gaps 2;

BASE COUNT 129 a 299 c 301 g 145 t

QY 1 GTGGCAGAAACACCCACTTACCTTGGCGGAGCAGACAGAGGAGCGGCTGTGTGC 60
Db 185 GTGGCAGAAACACCCACTTACCTTGGCGGAGCAGACAGAGGAGCGGCTGTGTGC 244
QY 61 GCCAGTGTGCCCCCAGGACCTTGTGACAGGCGCGGCGCGGAGCAGACCCACAGC 120
Db 245 GCCAGTGTGCCCCCAGGACCTTGTGACAGGCGCGGCGCGGAGCAGACCCACAGC 304
QY 121 TGTGCGCCGTGTCCACCGCCACTACACGACGTTCTGAACTACGTCGACGCTGCGC 180
Db 305 TGTGCGCCGTGTCCACCGCCACTACACGACGTTCTGAACTACGTCGACGCTGCGC 364
QY 181 TACTGCAAGTCTCTGTGCGGAGAGCTGAGAGAGAGCAGCGCTTGTGACCCAC 240
Db 365 TACTGCAAGTCTCTGTGCGGAGAGCTGAGAGAGAGCAGCGCTTGTGACCCAC 424
QY 241 AACCGTGTGCG 300
Db 425 AACCGTGTGCG 484
QY 301 GCATGTCCTCACCCTGTCGCGGCTGCTGATTTGCCCGGAGCACCCAGCAGAACACG 360
Db 485 GCATGTCCTCACCCTGTCGCGGCTGCTGATTTGCCCGGAGCACCCAGCAGAACACG 544
QY 361 TGCACGCGTGTGCCCCCGAGGACCTTGTGACGAGCTTCAAGAGCTGAGAGCTG 420
Db 545 TGCACGCGTGTGCCCCCGAGGACCTTGTGACGAGCTTCAAGAGCTGAGAGCTG 604
QY 421 CCCCACGCGCACTGACGCGGCTGAGGCTGGGCTGCTCATATGTGCAAGGCTTCTTCCCAT 480
Db 605 CCCCACGCGCACTGACGCGGCTGAGGCTGGGCTGCTCATATGTGCAAGGCTTCTTCCCAT 663
QY 481 GACACCTGTGACACGAGCTGACGCTGCTTCCCTCAGACAGGAGTACAGAGAGCTGAG 540
Db 664 GACACCTGTGACACGAGCTGACGCTGCTTCCCTCAGCA-CAGGATACAGAGATTATG 722
QY 541 GAGTGTGAGCGTGCCTGATGACTTGTGCTTTCAGAGACATCTCATCAAGAGCTG 600
Db 723 AAGTGTGAGCGTGCCTGATGACTTGTGCTTTCAGAGACATCTCATCAAGAGCTG 782
QY 601 CAGCGCTGTGTGACAGGCGCTTGTGAGGCGCGGAGGCTGGGCTGCCAGC 647
Db 783 GCGGTGTGTGAGCGCTTGTGAGGCGCGGAGGCTGGGCTGCCAGCAGGCGCGCGC 829

RESULT 10
AM083241/c
LOCUS AM083241 692 bp mRNA linear EST 14-OCT-1999
DEFINITION xc07a04.x1 NCI CGAP Co21 Homo sapiens cDNA clone IMAGE:2583534 3'
similar to TR_095407 O95407 DECOY RECEPTOR 3. :contains 11.b1 MBR22
repetitive element ;, mRNA sequence.

ACCESSION AM083241 GI:6038393
VERSION AM083241.1
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
human.
Mammalia; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 692)
NCI_CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The I.M.A.G.E. Consortium DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco
High quality sequence stop: 414.
Location/Qualifiers
1. .692
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="IMAGE:2583534"
/clone_lib="NCI CGAP Co21"
/tissue_type="moderately differentiated adenocarcinoma"
/lab_host="DH10B"
/notes="Organ: colon; Vector: pCMV-SPORT6; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt. Normalized to Cot >500. Average insert size 1.04kb. Normalized version of NCI_CGAP_Co18. Library constructed by Life Technologies."
BASE COUNT 136 a 205 c 235 g 115 t 1 others
ORIGIN
Query Match 59.4%; Score 482.6; DB 10; Length 692;
Best Local Similarity 97.7%; Pred. No. 9.1e-81;
Matches 510; Conservative 0; Mismatches 10; Indels 2; Gaps 2;
QY 293 TGGAGCAGCATCGTGTCCACCTGTGGTGGCGGTGATGTCGCCGGGACCCCGGCGAGA 352
Db 619 TGGAGCAGCATCGTGTCCACCT-GTCCGGCGGTGATGTCGCCGGGACCCCGGCGAGA 561
QY 353 ACAGGAGTCCAGCGTGTGCCCGGCGGACCTTCTCAGCAGCAGCTCCAGCTCAGC 412
Db 560 ACAGCAGTCCAGCGTGTGCCCGGCGGACCTTCTCAGCAGCAGCTCCAGCTCAGC 501
QY 413 AGTGCCAGCCCGCAGCACTGCACGCGCTTGGGCGCTTCAATGTGCCAGGCTCTT 472
Db 500 AGTGCCAGCCCGCAGCACTGCACGCGCTTGGGCGCTTCAATGTGCCAGGCTCTT 441
QY 473 CTTCCCATGACACCTGTGCACAGCTGCATCGACTTTGGGCTTTCCAGGACATCTCCATCA 532
Db 440 CTTCCCATGACACCTGTGCACAGCTGCATCGACTTTGGGCTTTCCAGGACATCTCCATCA 381
QY 533 GAGCTGAGGAGTGACGCTGCGGTATCGACTTTGGGCTTTCCAGGACATCTCCATCA 592
Db 380 GAGCTGAGGAGTGACGCTGCGGTATCGACTTTGGGCTTTCCAGGACATCTCCATCA 321
QY 593 AGAGGCTGACGCGCTCTCTCAGCGCTTGCAGGCGCCGAGGGGTGGGGTCCGACACAA 652
Db 320 AGAGGCTGACGCGCTCTCTCAGCGCTTGCAGGCGCCGAGGGGTGGGGTCCGACACAA 261
QY 653 GGGCGGCGCGGGCGCTTTCAGCTGAAGC-TGCGTCCGGCGGTTCACGAGCTCTTGGGG 711
Db 260 GGGCGGCGCGGGCGCTTTCAGCTGAAGC-TGCGTCCGGCGGTTCACGAGCTCTTGGGG 201
QY 712 GCGCAGACGGGGCGCTGTGTGGGCTGTGTGCGGCTGTGTGCGGCTGTGTGCGGCTGTGTG 771
Db 200 GCGCAGACGGGGCGCTGTGTGGGCTGTGTGCGGCTGTGTGCGGCTGTGTGCGGCTGTGTG 141
QY 772 GGGCTGAGCGGAGCGCTGTGTGCGGCTGTGTGCGGCTGTGTGCGGCTGTGTGCGGCTGTGTG 813
Db 140 GGGCTGAGCGGAGCGCTGTGTGCGGCTGTGTGCGGCTGTGTGCGGCTGTGTGCGGCTGTGTG

similar to TR:095407 095407 DECOY RECEPTOR 3. ; contains TAR1.b1
TAR1 repetitive element ; mRNA sequence.
ACCESSION AW262121.1 GI:6638937
VERSION AW262121.1
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 600)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The I.M.A.G.E. Consortium DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Possible reversed clone: polyT not found
Seq primer: -40UP from Gibco
High quality sequence stop: 410.
Location/Qualifiers
1. .600
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="IMAGE:2752231"
/clone_lib="NCI CGAP Lu28"
/tissue_type="two pooled squamous cell carcinomas"
/lab_host="DH10B"
/notes="Organ: lung; Vector: pCMV-SPORT6; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt. Library constructed by Life Technologies."
BASE COUNT 120 a 177 c 199 g 102 t 2 others
ORIGIN
Query Match 57.4%; Score 466.8; DB 10; Length 600;
Best Local Similarity 98.1%; Pred. No. 8.1e-78;
Matches 471; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 334 CCGGGCAGCCCGCAGCAACACGAGTCCAGCGCTGCCCGGCGGACCTTCTCAGCC 393
Db 600 CCGGGCAGCCCGCAGCAACACGAGTCCAGCGCTGCCCGGCGGACCTTCTCAGCC 541
QY 394 AGCAGCTCAGCTCAGAGCAGTCCAGCGCCCGCAGCAACTGCAACGCGCTTGGGCTGGCC 453
Db 540 AGCAGCTCAGCTCAGAGCAGTCCAGCGCCCGCAGCAACTGCAACGCGCTTGGGCTGGCC 481
QY 454 CTCATGTGCCAGGCTTCTCTCCCATGACCCCTGTGTGACAGCTGACAGCTTCCCC 513
Db 480 CTCATGTGCCAGGCTTCTCTCCCATGACCCCTGTGTGACAGCTGACAGCTTCCCC 421
QY 514 CTCAGCACAGGGTACAGGAGCTGAGGAGTGTGAGCGTGCCTCATCGACTTTGTGGCT 573
Db 420 CTCAGCACAGGGTACAGGAGCTGAGGAGTGTGAGCGTGCCTCATCGACTTTGTGGCT 361
QY 574 TTCAGGACATCTCCATCAAGAGGCTGACGCGCTCTCTCAGCGCTTCTCAGCGCTTCCCC 633
Db 360 TTCAGGACATCTCCATCAAGAGGCTGACGCGCTCTCTCAGCGCTTCTCAGCGCTTCCCC 301
QY 634 GGCTGGGTCCGACACAGAGGGGGCGCGCGGCTTTCAGCTGAAGCTGCTGCGCGG 693
Db 300 GGCTGGGTCCGACACAGAGGGGGCGCGCGGCTTTCAGCTGAAGCTGCTGCGCGG 241
QY 694 CTCACGAGCTCTCTGGGGGCGAGGACGGGGCGCTCTGTGTGGGCTGTGTGACGGGCTG 753
Db 240 CTCACGAGCTCTCTGGGGGCGAGGACGGGGCGCTCTGTGTGGGCTGTGTGACGGGCTG 181

RESULT 11
AW262121/c 600 bp mRNA linear EST 28-DEC-1999
LOCUS AW262121
DEFINITION xq31a04.x1 NCI_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2752231.3'

QY 754 CGCGTGGCCAGATGCGCGGCTGAGCGGAGCGTCCGTGAGCGCTTCTCCCTGTGCAC 813
 DB 180 CGCGTGGCCAGATGCGCGGCTGAGCGGAGCGTCCGTGAGCGCTTCTCCCTGTGCAC 121

RESULT 12
 BQ019285 568 bp mRNA linear EST 17-JUN-2002
 LOCUS BQ019285/c
 DEFINITION UI-H-DT1-awn-1-19-0-UI-61 NCI CGAP DT1 Homo sapiens cDNA clone
 IMAGE:5891874 3', mRNA sequence.
 accession BQ019285
 version BQ019285.1 GI:19754562
 keywords EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 568)
 NCBI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 TITLE Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Dr. Jose Mercuende
 cDNA library preparation: Dr. M. Bento Soares, University of Iowa
 DNA library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
 Seq primer: M13 FORWARD
 POLYA=Yes.

FEATURES
 source Location/Qualifiers
 1..568
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:5891874"
 /clone_1lb="NCI CGAP DT1"
 /issue_type="Metastatic Chondrosarcoma"
 /dev_stage="Adult"
 /lab_host="DH10B (Life Technologies)"
 /note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a
 modified polylinker; Site 1: EcoR I; Site 2: Not I;
 NCI CGAP DT1 is a normalized cDNA library containing the
 following tissue(s): Metastatic Chondrosarcoma in lung.
 The library was constructed according to Bonaldo, Lennon
 and Soares, Genome Research, 6:791-806, 1996. First strand
 cDNA synthesis was primed with an oligo-dT primer
 containing a Not I site. Double stranded cDNA was ligated
 to an EcoR I adaptor, digested with Not I, and cloned
 directionally into pT73-Pac vector. The oligonucleotide
 used to prime the synthesis of first-strand cDNA contains
 a library tag sequence that is located between the Not I
 site and the (dT)18 tail. The sequence tag for this
 library is AACTGTTCG.
 TAG_LIB=UI-H-DT1
 TAG_TISSUE=Lung metastatic chondrosarcoma
 TAG_SEQ=AACTGTTCG"

BASE COUNT 106 a 170 c 187 g 105 t

ORIGIN
 Query Match 56.3%; Score 458; DB 14; Length 568;
 Best Local Similarity 100.0%; Pred. No. 3.6e-76;
 Matches 458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 356 CGAGTGCACGCGTGCCTCCAGGACGCTTCTCAGCAGAGCTCCAGCTCAGAGCAGT 415
 DB 568 CGAGTGCACGCGTGCCTCCAGGACGCTTCTCAGCAGAGCTCCAGCTCAGAGCAGT 509

QY 416 GCCAGCCCAACCGCACTGACAGCGGCTCTGGGCTGCGCTTCAATGTGCGAGGCTTTCT 475
 DB 508 GCCAGCCCAACCGCACTGACAGCGGCTCTGGGCTCTTCAATGTGCGAGGCTTTCT 449

QY 476 CCCATGACACCCCTGTGCACACGAGCTGCTTCCCTCAGACACAGGTAACGAGAG 535
 DB 448 CCCATGACACCCCTGTGCACACGAGCTGCTTCCCTCAGACACAGGTAACGAGAG 389

QY 536 CTGAGAGTGTGAGCGCTGCCGTATCATCTTGTGCTTTCCAGACATCTCCATCAAGA 595
 DB 388 CTGAGAGTGTGAGCGCTGCCGTATCATCTTGTGCTTTCCAGACATCTCCATCAAGA 329

QY 596 GGTGAGAGGCGCTGACAGGCGCTGAGAGCCCGGAGGCGTGGGTTCCGACACCAAGG 655
 DB 328 GGTGAGAGGCGCTGACAGGCGCTGAGAGCCCGGAGGCGTGGGTTCCGACACCAAGG 269

QY 656 CGGCGCGCGGCGCTTGCAGACTGAAGCTGCTGCGCGCTCAACGAGACTCTTGGGGCGC 715
 DB 268 CGGCGCGCGGCGCTTGCAGACTGAAGCTGCTGCGCGCTCAACGAGACTCTTGGGGCGC 209

QY 716 AGGACGGGCGCTGCTGTGTGCGGCTCTGAGAGCGCTTGGCGGCTCCAGAGTCCCGGC 775
 DB 208 AGGACGGGCGCTGCTGTGTGCGGCTCTGAGAGCGCTTGGCGGCTCCAGAGTCCCGGC 149

QY 776 TGGAGCGAGCGCTGCGTGCAGCGCTTCTCCCTGTGCAC 813
 DB 148 TGGAGCGAGCGCTGCGTGCAGCGCTTCTCCCTGTGCAC 111

RESULT 13
 B1838357 588 bp mRNA linear EST 04-OCT-2001
 LOCUS B1838357
 DEFINITION 603083306F1 NIH_MGC_120 Homo sapiens cDNA clone IMAGE:5222545 5',
 mRNA sequence.
 accession B1838357
 version B1838357.1 GI:15949907
 keywords EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 588)
 NIH-MGC http://mgc.ncbi.nlm.nih.gov/
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE Unpublished (1999)
 JOURNAL Contact: Robert Strausberg, Ph.D.
 COMMENT Email: cgapbs-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA library preparation: Life Technologies, Inc.
 DNA library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LNA11559 row: 1 column: 02
 High quality sequence stop: 588.

FEATURES
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 /clone="IMAGE:5222545"
 /clone_1lb="NIH_MGC_120"
 /lab_host="DH10B"
 /note="Organ: pooled pancreas and spleen; Vector:
 pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA
 source anonymous pool of spleen and pancreas from 28 yo
 male. Library is oligo-dT primed and directionally cloned
 (EcoRV site is destroyed upon cloning). Average insert
 size 1.5 kb, insert size range 1-2.5 kb. Library is
 normalized and enriched for full-length clones and was
 constructed by C. Gruber (Invitrogen) Research Genetics
 tracking code 025. Note: this is a NIH_MGC library."

BASE COUNT 97 a 224 c 171 g 95 t

ORIGIN
 Query Match 52.7%; Score 428.6; DB 13; Length 588;

Best Local Similarity 98.9%; Pred. No. 1.1e-70; Mismatches 5; Indels 0; Gaps 0; Matches 431; Conservative 0;

QY 100 CGCCGAGACAGCCCGACGCTGTGGCCCTGTCCACCGCGCCACTACAGCGATTTCTGG 159
Db 1 CGCCGAGACAGCCCGACGCTGTGGCCCTGTCCACCGCGCCACTACAGCGATTTCTGG 60

QY 160 AACTTACTGAGCGCTGCCGCTACTGTCAAGCTCTTTCGGGGAGCGCTGAGGAGGCA 219
Db 61 AACTTACTGAGCGCTGCCGCTACTGTCAAGCTCTTTCGGGGAGCGCTGAGGAGGCA 120

QY 220 CGGGCTTGCCACGCCACCCACGCTGCTGCGCTGCGCGCCGCGCTTCTTTCGGCGAC 279
Db 121 CGGGCTTGCCACGCCACCCACGCTGCTGCGCTGCGCGCCGCGCTTCTTTCGGCGAC 180

QY 280 GCTGTTTCTGTTGGAGCAGCATCTGTCACCTGCTGCGCGCTGATTTGCCCGCGGC 339
Db 181 GCTGTTTCTGTTGGAGCAGCATCTGTCACCTGCTGCGCGCTGATTTGCCCGCGGC 240

QY 340 ACCCCAGCCAGAAACAGCGAGTGCACCGCTGCGCCCGCCAGGCACTTCTCAGCCAGC 399
Db 241 ACCCCAGCCAGAAACAGCGAGTGCACCGCTGCGCCCGCCAGGCACTTCTCAGCCAGC 300

QY 400 TCCAGCTCAGAGCAGTGCACCGCCACCGCACTGCGCGCTGCGCGCTGCGCGCTCAAT 459
Db 301 TCCAGCTCAGAGCAGTGCACCGCCACCGCACTGCGCGCTGCGCGCTGCGCGCTCAAT 360

QY 460 GTCCAGGCTTCTTCTCCCATGACACCTGTGACACGCTGCTGCGCTTCCCGCTCAGC 519
Db 361 GTCCAGGCTTCTTCTCCCATGACACCTGTGACACGCTGCTGCGCTTCCCGCTCAGC 420

QY 520 ACCAGGTTACAGGAG 535
Db 421 ACCAGGTTACAGGAG 436

RESULT 14
BE879166 601486906F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3889296 5',
LOCUS mRNA sequence.
DEFINITION BE879166.1 GI:10327942
ACCESSION BE879166
VERSION BE879166
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE NIH-MGC http://mgc.nci.nih.gov/.
AUTHORS 1 (bases 1 to 551)
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM9670 row: 1 column: 01
High quality sequence stop: 546.
Location/Qualifiers
1. .551
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/db_xref="taxon:9606"
/clone="IMAGE:3889296"
/clone_lib="NIH MGC 69"
/tissue_types="large cell carcinoma, undifferentiated"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lung; Vector: pCMV-Sport6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.

Average insert size 1.1 kb. Library constructed by Life Technologies." 76 a 189 c 190 g 96 t

Query Match 51.9%; Score 421.6; DB 12; Length 551;
Best Local Similarity 98.7%; Pred. No. 2.3e-69; Mismatches 4; Indels 2; Gaps 2;
Matches 446; Conservative 0;

QY 363 CCAGCCGTGCCCCCAGGCACTTCTCAGCCAGCAGCTCCAGCTCAGAGAGTGCAGCC 422
Db 80 CGATGCTGTCTCCCGAGGCACTTCTCAGCCAGCAGCTCCAGCTCAGAGAGTGCAGCC 139

QY 423 CACCCGAACTGACAGCGCCCTGGGCTGCGCTCAATGTGCCAGGCTTCTTCTCCCATGA 482
Db 140 CACCCGAACTGACAGCGCCCTGGGCTGCGCTCAATGTGCCAGGCTTCTTCTCCCATGA 198

QY 483 CACCCGTGACACGAGTGCACCTGCTTCCCTCAGCACCGAGGTACAGGAGCTGAGGA 542
Db 199 CACCCGTGACACGAGTGCACCTGCTTCCCTCAGCACCGAGGTACAGGAGCTGAGGA 258

QY 543 GTGTGAGCGTGCCTGCATCGACTTTTGTGGCTTTCAGGACATCTCCATCAAGAGGCTGCA 602
Db 259 GTGTGAGCGTGCCTGCATCGACTTTTGTGGCTTTCAGGACATCTCCATCAAGAGGCTGCA 318

QY 603 GCGGCTGTGACAGCGCTCGAGGCCCGGAGGCTGGGTCCGACACCAAGAGGCGGCGC 662
Db 319 GCGGCTGTGACAGCGCTCGAGGCCCGGAGGCTGGGTCCGACACCAAGAGGCGGCGC 378

QY 663 CGCGGCTTTCAGCTCAAGCTGCTGCGGCTCAGCGAGCTCCTGGGGCGCAGGACGG 722
Db 379 CGCGGCTTTCAGCTCAAGCTGCTGCGGCTCAGCGAGCTCCTGGGGCGCAGGACGG 438

QY 723 GCGGCTGTGCTGCGGCTGCTGCAGGCGCTGCGCTGGCCAGGATGCCGGGCTGGAGCG 782
Db 439 GCGGCTGTGCTGCGGCTGCTGCAGGCGCTGCGCTGGCCAGGATGCCGGGCTGGAGCG 498

QY 783 GAGC-GTCCGTGAGCGCTTCTCCCTGTGCGAC 813
Db 499 GAGCAGTCCGTGAGCGCTTCTCCCTGTGCGAC 530

RESULT 15
AW471440/C
LOCUS
DEFINITION xw59e06.x1 NCI CGAP Pan1 Homo sapiens cDNA clone IMAGE:283232 3',
similar to TR:095407 O95407 DECOY RECEPTOR 3. ; contains TAR1.b1
TAR1 repetitive element ;, mRNA sequence.
ACCESSION AW471440
VERSION AW471440.1 GI:7041546
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS 1 (bases 1 to 540)
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Life Technologies catalog #: 11548-013
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco
High quality sequence stop: 387.
Location/Qualifiers
1. .540
/organism="Homo sapiens"
/db_xref="taxon:9606"

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/clone="IMAGE:2832322"
/clone_lib="NCI CGAP Pan1"
/tissue_type="adenocarcinoma"
/lab_host="VDH0B"
/notes="Organ: pancreas; Vector: pCMV-Sport6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.72 kb. Life Technologies catalog #:
11548-013"

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/cissue_type="adenocarcinoma"
/lab_host="DH10B"
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/note="Organ: pan
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Average insert size 1.72 kb. Life Technologies catalog #: site 2: NOC1; cloned unidirectionally. primer: origo di.

BASE COUNT ORIGIN	120 a	165 c	160 g	88 t	7 others
----------------------	-------	-------	-------	------	----------

ORIGIN

Query Match

Best Local Similarity 95.2%; Pred. No. 1.7e-67;
Matches 420; Concordance 0.91; Mismatches 31

Matches 420; conservative 0; mismatches 21; indels 0; gaps 0;

Qy	373	CCCCAGGACCTTCTCAGCCAGAGCTCCAGCTCAAGCAGTGCAGGCCACCGCAAC	4322
Db	540	CTTTAGGMACTTTTCTCAGCTAGTAGCTCCAGCTTAAGTAGTAGTCCGCCACTGTAA	481
Qy	433	TGCACGGCTCTGGGCTGGGCTCTCAATGTGTGCAGGCTCTTCTCCATGACACCTGTGC	4922
Db	480	TGTATGGCCNNTGGCCNNTGGCCCTCAATGTGTGACAGGCTCTTCTCCATGTACACCNNTGTC	421
Qy	493	ACCAAGCTGCACTGGCTTCCCTCAGGACCAAGGGGTACCAAGAGCTGAGAGTGTGAGCGT	5522
Db	420	ACCAAGNTGCACTGGCTTCCCTCAGGACCAAGGGGTACCAAGAGTGTGAGAGTGTGAGCGT	361
Qy	553	GCCGTCATCGACTTTGTGTGGCTTTTCAGAGACATCTTCATCAAGAGGCTGCAGCGGCTGCTG	6122
Db	360	GCCGTCATCGACTTTGTGTGGCTTTTCAGAGACATCTTCATCAAGAGGCTGCAGCGGCTGCTG	301
Qy	613	CAGGCTCTTCAGAGGCCCGCGAGAGGGCTGGGGTCCAGACACCAAGAGGCTGGGCGCGGCTTG	6722
Db	300	CAGGCTCTTCAGAGGCCCGCGAGAGGGCTGGGGTCCAGACACCAAGAGGCTGGGCGCGGCTTG	241
Qy	673	CAGCTGAAGCTGCGTCCGGCGGCTCAGCGAGCTCTCTGGGGGGCGCAGACCGGGCGCTGCTG	7322
Db	240	CAGCTGAAGCTGCGTCCGGCGGCTCAGCGAGCTCTCTGGGGGGCGCAGACCGGGCGCTGCTG	181
Qy	733	GTCGCGGCTGTGCAGAGCGCTGCAGTGTGCAGATGCTCCGGGCTGAGCGGAGCGTCCGT	7922
Db	180	GTCGCGGCTGTGCAGAGCGCTGCAGTGTGCAGATGCTCCGGGCTGAGCGGAGCGTCCGT	121
Qy	793	GAGCGCTTCCCTCCCTGTGTGCAC	813
Db	120	GAGCGCTTCCCTCCCTGTGTGCAC	100

Db 540 CCTTAGNACTTCTCAGCTAGCTCCAGCTTAGAGTAGTGCTAGCCCCACTGTAA 481

Qy 433 TGCACGGCCCTGGGACCTCAATGTGGCAGGCTCTTCTCCCATGACACACCTGTGC 4992

Db 480 TGTATGGCNCNTGGGACCTCAATGTGNCAGGCTCTTCTTCCCATGACACACNTGTGC 421

493 ACCAGCTGCACTGGCTTCCCCCTCAGACCAAGGTAACAGAGCTGAGAGTGTGAGCGT 552

D6 420 ACCAGTGCACCTGGCTTCCCTCCAGCACCCAGGTAACGAGAGCTGAAGAGTGTACGCGT 361

QY 553 GCCGTATCGACTTTGTGGCTTTCAGACATCTCCATCAAGAGGCTGACGGCGTCTG 6122

Db 360 GCCGTCATCGACTTGTGGCTTCCAGACATCTTCATCAAGAGGCTGCAGCGGCTGT 301

613 CAGGCCCTCGAGGCCCGGAGGAGCTGGGATCCGACACCAAGGAGGCGCGCGCTTG 672
 |||||
 300 CAGGCCCTCGAGGCCCGGAGGAGCTGGGATCCGACACCAAGGAGGCGCGCGCTTG 241

673 CAGCTGAAGCTGCGTCGGCGGCTACGGAGCTCTGGGGGGCGAGGACGGGGCGCTGCTG 732

D5 240 CAGCAGAGCAGCGGCTGCACGGAGATCCGTGGGGGGCAGGACGGGGGCCGACGCG 181

OY 733 GTGCGGCTGCAAGGCGGCTGCAGGATGCCCGGCTTGAGCGGAGCGTCCTT 792

Db 180 GTGCGCTGCTGCAAGGCGCTGCGCGTGCCACGATGCCCCGGCTGAGCGGAGCGTCCGT 121

97 755 GAGCGCAGCCCGCCCGCGAC 813
 |||||
 Db 120 GAGCGCTTCCTCCCTGTGCAC 100

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Job time: 1973.0000

000 CTIME : 17/3 SEC8

Search completed: January 6, 2003, 15:13:25
Job time : 1973 secs

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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: January 6, 2003, 13:48:11 ; Search time 54 Seconds
(without alignments)
4617.189 Million cell updates/sec

Title: US-09-936-024-2

Perfect score: 813
Sequence: 1 gfcgcagaacaccaccacta.....agcgcctccctccctgacac 813

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents NA: *
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2: /cgn2_6/prodata/2/ina/5B COMB.seq: *
3: /cgn2_6/prodata/2/ina/6A COMB.seq: *
4: /cgn2_6/prodata/2/ina/6B COMB.seq: *
5: /cgn2_6/prodata/2/ina/PCTUS COMB.seq: *
6: /cgn2_6/prodata/2/ina/backtitles1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	813	100.0	1164	2	US-08-794-796-1	Sequence 1, Appl1
2	813	100.0	1347	4	US-09-286-529-18	Sequence 18, Appl1
3	533.4	65.6	1859	4	US-09-286-529-19	Sequence 19, Appl1
4	459	56.5	459	4	US-09-286-529-7	Sequence 7, Appl1
5	129.6	15.9	525	3	US-08-997-918-47	Sequence 47, Appl1
6	112	13.8	2432	3	US-08-974-022-1	Sequence 1, Appl1
7	112	13.8	2432	4	US-08-795-445A-1	Sequence 1, Appl1
8	112	13.8	2432	4	US-08-795-447A-1	Sequence 1, Appl1
9	112	13.8	2432	4	US-08-974-186-1	Sequence 1, Appl1
10	112	13.8	2432	4	US-08-795-446B-1	Sequence 1, Appl1
11	112	13.8	2432	4	US-08-706-945D-123	Sequence 123, Appl1
12	110.4	13.6	1324	3	US-08-974-022-3	Sequence 3, Appl1
13	110.4	13.6	1324	4	US-08-795-445A-3	Sequence 3, Appl1
14	110.4	13.6	1324	4	US-08-795-447A-3	Sequence 3, Appl1
15	110.4	13.6	1324	4	US-08-974-186-3	Sequence 3, Appl1
16	110.4	13.6	1324	4	US-08-795-446B-3	Sequence 3, Appl1
17	110.4	13.6	1324	4	US-08-706-945D-125	Sequence 125, Appl1
18	103	12.7	1355	3	US-08-974-022-5	Sequence 5, Appl1
19	103	12.7	1355	4	US-08-795-445A-5	Sequence 5, Appl1
20	103	12.7	1355	4	US-08-795-447A-5	Sequence 5, Appl1
21	103	12.7	1355	4	US-08-974-186-5	Sequence 5, Appl1
22	103	12.7	1355	4	US-08-795-446B-5	Sequence 5, Appl1
23	103	12.7	1355	4	US-08-706-945D-127	Sequence 127, Appl1
24	76	9.3	3331	4	US-09-042-785A-1	Sequence 1, Appl1
25	68	8.4	759	4	US-09-042-785A-6	Sequence 6, Appl1
26	68	8.4	1815	4	US-09-042-785A-24	Sequence 24, Appl1
27	68	8.4	2186	3	US-08-959-382-1	Sequence 1, Appl1

28	68	8.4	2612	4	US-09-042-785A-3	Sequence 3, Appl1
29	68	8.4	2638	4	US-09-042-785A-22	Sequence 22, Appl1
30	68	8.4	3474	4	US-09-527-236A-1	Sequence 1, Appl1
31	56.4	6.9	1719	4	US-09-042-785A-5	Sequence 5, Appl1
32	54.8	6.7	1164	2	US-08-794-796-1	Sequence 1, Appl1
33	54.8	6.7	1347	4	US-09-286-529-18	Sequence 18, Appl1
34	52	6.4	2793	1	US-08-209-747-1	Sequence 1, Appl1
35	52	6.4	2793	1	US-08-458-298-1	Sequence 1, Appl1
36	51.6	6.3	3796	2	US-08-762-308-11	Sequence 11, Appl1
37	51.6	6.3	3796	2	US-09-844-634-10	Sequence 10, Appl1
38	51.6	6.3	3813	2	US-08-650-000-3	Sequence 3, Appl1
39	51.6	6.3	3813	6	US-08-5395760-3	Sequence 3, Appl1
40	49.6	6.1	691	1	US-08-266-080B-12	Sequence 12, Appl1
41	49.6	6.1	691	5	PCT-US95-05423-12	Sequence 12, Appl1
42	49.6	6.1	705	4	US-09-326-394-3	Sequence 3, Appl1
43	48.6	6.1	8906	2	US-08-826-267-1	Sequence 1, Appl1
44	48.6	6.0	1878	3	US-08-966-139-14	Sequence 14, Appl1
45	48.6	6.0	1878	4	US-08-995-659-14	Sequence 14, Appl1

ALIGNMENTS

RESULT 1
US-08-794-796-1
; Sequence 1, Application US/08794796
; Patent No. 5885800
GENERAL INFORMATION:
; APPLICANT: Emery, John
; APPLICANT: Tan, KB
; APPLICANT: Truneh, Alem
; APPLICANT: Young, Peter
TITLE OF INVENTION: Tumor Necrosis Related Receptor,
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
City: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/794, 796
FILING DATE: 04-FEB-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Han, William T
REGISTRATION NUMBER: 34,344
REFERENCE/DOCKET NUMBER: GH50000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5219
TELEFAX: 610-270-4026
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1164 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-794-796-1
Query Match 100.0%; Score 813; DB 2; Length 1164;
Best Local Similarity 100.0%; Pred. No. 2.6e-154;

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Matches 813; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTGGCAGAAACACCCACCTACCCCTGGCGGAGCGAGACAGGGAGCGGCTGGTGTGC 60
Db 198 GTGGCAGAAACACCCACCTACCCCTGGCGGAGCGAGACAGGGAGCGGCTGGTGTGC 257
QY 61 GCCCAGTGGCCCCCAGGACCTTTGTGACGCGCGCTGGCCGAGACAGCCCCACGACG 120
Db 258 GCCCAGTGGCCCCCAGGACCTTTGTGACGCGCGCTGGCCGAGACAGCCCCACGACG 317
QY 121 TGTGGGCGGTGTCCACCGGCCACTACACGACGTTCTGGAATACCTTGGAGCGCTGCCGC 180
Db 318 TGTGGGCGGTGTCCACCGGCCACTACACGACGTTCTGGAATACCTTGGAGCGCTGCCGC 377
QY 181 TACTGCAACGTTCTTGTGGGGAGCGTGTAGGAGGAGCAGCGGCTTGCACAGCCACCCAC 240
Db 378 TACTGCAACGTTCTTGTGGGGAGCGTGTAGGAGGAGCAGCGGCTTGCACAGCCACCCAC 437
QY 241 AACCGTGCCTGCCGCTGCCGACCGGCTTCTTCCGACGCTGGTTTCTGCTTGGAGCAC 300
Db 438 AACCGTGCCTGCCGCTGCCGACCGGCTTCTTCCGACGCTGGTTTCTGCTTGGAGCAC 497
QY 301 GCATCGTGTCCACCTGTGGCGCGGTGATTGCCCGCGGACACCCCGCAGAACACGCGAG 360
Db 498 GCATCGTGTCCACCTGTGGTGC CGGGGTGATTGCCCGCGGACACCCCGCAGAACACGCGAG 557
QY 361 TGCAGCGGTGCCCGCCAGGACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 420
Db 558 TGCAGCGGTGCCCGCCAGGACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 617
QY 421 CCCACCGCAACTGCAGCGGCTTGGGCTTCCGCTCAGCACAGGGTACAGGAGCTGAG 480
Db 618 CCCACCGCAACTGCAGCGGCTTGGGCTTCCGCTCAGCACAGGGTACAGGAGCTGAG 677
QY 481 GACACCTGTGCACCACTGCTGCTTCCCTCAGCACAGGGTACAGGAGCTGAG 540
Db 678 GACACCTGTGCACCACTGCTGCTTCCCTCAGCACAGGGTACAGGAGCTGAG 737
QY 541 GAGTGTAGCGGTCCGCTATCGACTTGTGGCTTTCAGGACATCTCCATCAAGAGGCTG 600
Db 738 GAGTGTAGCGGTCCGCTATCGACTTGTGGCTTTCAGGACATCTCCATCAAGAGGCTG 797
QY 601 CAGCGGCTGTGCAGCGCTCAGGCGCCGCGAGGCTGGGGTCCGACACCAAGGGCGGC 660
Db 798 CAGCGGCTGTGCAGCGCTCAGGCGCCGCGAGGCTGGGGTCCGACACCAAGGGCGGC 857
QY 661 CGCGCGGCTTGCAGCTGAAGCTGCGTCCGCGGCTCAGCGAGCTCCTGGGGGCGCAGGAC 720
Db 858 CGCGCGGCTTGCAGCTGAAGCTGCGTCCGCGGCTCAGCGAGCTCCTGGGGGCGCAGGAC 917
QY 721 GGGGCGCTGTGTGGGCTGTGTGAGCGCTGCGGCTGCGCAGGATGCCCGGGCTGGAG 780
Db 918 GGGGCGCTGTGTGGGCTGTGTGAGCGCTGCGGCTGCGCAGGATGCCCGGGCTGGAG 977
QY 781 CGGAGCGCTCGTGCAGCGCTTCTCCCTGTGCAC 813
Db 978 CGGAGCGCTCGTGCAGCGCTTCTCCCTGTGCAC 1010
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RESULT 2

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US-09-286-529-18
; Sequence 18, Application US/09286529
; Patent No. 6297367
; GENERAL INFORMATION:
; APPLICANT: Catherine Tribouley
; TITLE OF INVENTION: NEW MEMBERS OF TNF AND TNFR FAMILIES
; FILE REFERENCE: 1408.003/200130.439C1
; CURRENT APPLICATION NUMBER: US/09/286,529
; CURRENT FILING DATE: 1999-04-05
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 18
; LENGTH: 1347
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; TYPE: DNA
; ORGANISM: Homo sapien
US-09-286-529-18
Query Match 100.0%; Score 813; DB 4; Length 1347;
Best Local Similarity 100.0%; Pred. No. 2.6e-154;
Matches 813; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTGGCAGAAACACCCACCTACCCCTGGCGGAGCGAGACAGGGAGCGGCTGGTGTGC 60
Db 405 GTGGCAGAAACACCCACCTACCCCTGGCGGAGCGAGACAGGGAGCGGCTGGTGTGC 464
QY 61 GCCCAGTGGCCCCCAGGACCTTTGTGACGCGCGCTGGCCGAGACAGCCCCACGACG 120
Db 465 GCCCAGTGGCCCCCAGGACCTTTGTGACGCGCGCTGGCCGAGACAGCCCCACGACG 524
QY 121 TGTGGGCGGTGTCCACCGGCCACTACACGACGTTCTGGAATACCTTGGAGCGCTGCCGC 180
Db 525 TGTGGGCGGTGTCCACCGGCCACTACACGACGTTCTGGAATACCTTGGAGCGCTGCCGC 584
QY 181 TACTGCAACGTTCTTGTGGGGAGCGTGTAGGAGGAGCAGCGGCTTGCACAGCCACCCAC 240
Db 585 TACTGCAACGTTCTTGTGGGGAGCGTGTAGGAGGAGCAGCGGCTTGCACAGCCACCCAC 644
QY 241 AACCGTGCCTGCCGCTGCCGACCGGCTTCTTCCGACGCTGGTTTCTGCTTGGAGCAC 300
Db 645 AACCGTGCCTGCCGCTGCCGACCGGCTTCTTCCGACGCTGGTTTCTGCTTGGAGCAC 704
QY 301 GCATCGTGTCCACCTGTGGCGCGGTGATTGCCCGCGGACACCCCGCAGAACACGCGAG 360
Db 705 GCATCGTGTCCACCTGTGGTGC CGGGGTGATTGCCCGCGGACACCCCGCAGAACACGCGAG 764
QY 361 TGCAGCGGTGCCCGCCAGGACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 420
Db 765 TGCAGCGGTGCCCGCCAGGACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 824
QY 421 CCCACCGCAACTGCAGCGGCTTGGGCTTCCGCTCAGCACAGGGTACAGGAGCTGAG 480
Db 825 CCCACCGCAACTGCAGCGGCTTGGGCTTCCGCTCAGCACAGGGTACAGGAGCTGAG 884
QY 481 GACACCTGTGCACCACTGCTGCTTCCCTCAGCACAGGGTACAGGAGCTGAG 540
Db 885 GACACCTGTGCACCACTGCTGCTTCCCTCAGCACAGGGTACAGGAGCTGAG 944
QY 541 GAGTGTAGCGGTCCGCTATCGACTTGTGGCTTTCAGGACATCTCCATCAAGAGGCTG 600
Db 945 GAGTGTAGCGGTCCGCTATCGACTTGTGGCTTTCAGGACATCTCCATCAAGAGGCTG 1004
QY 601 CAGCGGCTGTGCAGCGCTCAGGCGCCGCGAGGCTGGGGTCCGACACCAAGGGCGGC 660
Db 1005 CAGCGGCTGTGCAGCGCTCAGGCGCCGCGAGGCTGGGGTCCGACACCAAGGGCGGC 1064
QY 661 CGCGCGGCTTGCAGCTGAAGCTGCGTCCGCGGCTCAGCGAGCTCCTGGGGGCGCAGGAC 720
Db 1065 CGCGCGGCTTGCAGCTGAAGCTGCGTCCGCGGCTCAGCGAGCTCCTGGGGGCGCAGGAC 1124
QY 721 GGGGCGCTGTGTGGGCTGTGTGAGCGCTGCGGCTGCGCAGGATGCCCGGGCTGGAG 780
Db 1125 GGGGCGCTGTGTGGGCTGTGTGAGCGCTGCGGCTGCGCAGGATGCCCGGGCTGGAG 1184
QY 781 CGGAGCGCTCGTGCAGCGCTTCTCCCTGTGCAC 813
Db 1185 CGGAGCGCTCGTGCAGCGCTTCTCCCTGTGCAC 1217
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RESULT 3

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US-09-286-529-19
; Sequence 19, Application US/09286529
; Patent No. 6297367
; GENERAL INFORMATION:
; APPLICANT: Catherine Tribouley
; TITLE OF INVENTION: NEW MEMBERS OF TNF AND TNFR FAMILIES
; FILE REFERENCE: 1408.003/200130.439C1
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TOPOLOGY: linear
 MOLECULE TYPE: CDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 124..1326
 US-08-795-445A-1

Query Match 13.8%; Score 112; DB 4; Length 2432;
 Best Local Similarity 52.3%; Pred. No. 2.8e-14;
 Matches 247; Conservative 0; Mismatches 225; Indels 0; Gaps 0;

QY 31 GACGACAGACAGGGGAGCGGCTGTGTGCGCCAGTGCCTCCAGCACCCTTTGTGACG 90
 DB 217 GACCCAGAAAACCGAGCTGAGCTTGTGTGACCAATGTGTCTCTGACACTACTATAAA 276
 QY 91 CGGCGGCGCGCGCGAGACAGCCCAAGCAGTGTGCGCGGTGTCCACCGCGCACTAACAG 150
 DB 277 CAGCAGTGCACAGTCAAGAGAGAAACAGTGTGTCTCTGCGCTGACTACTTATPACA 336
 QY 151 CAGTTCTGAACTACTGAGCGCTGCGCTACTGCAACGTCCTCTGCGGAGACGTGAG 210
 DB 337 GACAGCTGGACACAGATGATGATGTGTACTGACGCCCCGTGTGCAAGAACTGCAG 396
 QY 211 GAGAGGACAGGGCTTGTCCACGCCACCAACCGTGTGCGCTGCGCGTCCGACCGGCTTC 270
 DB 397 ACCGTGAAACAGAGAGTGAACCCGACCAACCGAGTGTGCAATGTGAGAAAGGGCGC 456
 QY 271 TTGCGGACGCTGTGTCTGTGTGTGAGACAGCATGTGTCCACTGTGTGCGGTGAT 330
 DB 457 TACCTGAGCTCGAATTTCTGTGAAACCGAGCTGTCTCCCGAGCTTGTGTGTCTG 516
 QY 331 GCCCGGGGACCCCGACCGCAAGACAGCAGTGCAGCGCTGCGCGCGCGGACCTTCTCA 390
 DB 517 CAGGCTGGACCCCGAGAGCAACAGCTTGTGCAAAAGATGTCCGATGGGTTTCTTCA 576
 QY 391 GCCAGCAGCTCCAGCTCAGAGCAGTGCAGCGCCGCAACCTGACAGCGCTGTGGCGTG 450
 DB 577 GGTGAGACGTGATGAAAGACCCCTGTAGGAAACACACCAACTGACACTGCTGGGCTC 636
 QY 451 GCCCTCATGTGCGAGGCTTCTCTCCATGACACCTGTGACACAGCTGCA 502
 DB 637 CTGCTAATTCAGAAAGAAATGCAACACATGACATGTATGTTCGGAAACA 688

RESULT 8
 US-08-795-447A-1
 Sequence 1, Application US/08795447A
 Patent No. 6284728

GENERAL INFORMATION:
 APPLICANT: Boyle, William J.
 APPLICANT: Lacey, David L.
 APPLICANT: Calzone, Frank J.
 APPLICANT: Chang, Ming-Shi
 TITLE OF INVENTION: Osteoprotegerin
 NUMBER OF SEQUENCES: 53
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Amgen Inc.
 STREET: One Amgen Center Drive
 CITY: Thousand Oaks
 STATE: California
 COUNTRY: USA
 ZIP: 91362-1789
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/795.447A
 FILING DATE:
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Winter, Robert B.

REFERENCE/DOCKET NUMBER: A-37802
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2432 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: CDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 124..1326
 US-08-795-447A-1

Query Match 13.8%; Score 112; DB 4; Length 2432;
 Best Local Similarity 52.3%; Pred. No. 2.8e-14;
 Matches 247; Conservative 0; Mismatches 225; Indels 0; Gaps 0;

QY 31 GACGACAGACAGGGGAGCGGCTGTGTGCGCCAGTGCCTCCAGCACCCTTTGTGACG 90
 DB 217 GACCCAGAAAACCGAGCTGAGCTTGTGTGACCAATGTGTCTCTGACACTACTATAAA 276
 QY 91 CGGCGGCGCGCGCGAGACAGCCCAAGCAGTGTGCGCGGTGTCCACCGCGCACTAACAG 150
 DB 277 CAGCAGTGCACAGTCAAGAGAGAAACAGTGTGTCTCTGCGCTGACTACTTATPACA 336
 QY 151 CAGTTCTGAACTACTGAGCGCTGCGCTACTGCAACGTCCTCTGCGGAGACGTGAG 210
 DB 337 GACAGCTGGACACAGATGATGATGTGTACTGACGCCCCGTGTGCAAGAACTGCAG 396
 QY 211 GAGAGGACAGGGCTTGTCCACGCCACCAACCGTGTGCGCTGCGCGTCCGACCGGCTTC 270
 DB 397 ACCGTGAAACAGAGAGTGAACCCGACCAACCGAGTGTGCAATGTGAGAAAGGGCGC 456
 QY 271 TTGCGGACGCTGTGTCTGTGTGTGAGACAGCATGTGTCCACTGTGTGCGGTGAT 330
 DB 457 TACCTGAGCTCGAATTTCTGTGAAACCGAGCTGTCTCCCGAGCTTGTGTGTCTG 516
 QY 331 GCCCGGGGACCCCGACCGCAAGACAGCAGTGCAGCGCTGCGCGCGCGGACCTTCTCA 390
 DB 517 CAGGCTGGACCCCGAGAGCAACAGCTTGTGCAAAAGATGTCCGATGGGTTTCTTCA 576
 QY 391 GCCAGCAGCTCCAGCTCAGAGCAGTGCAGCGCCGCAACCTGACAGCGCTGTGGCGTG 450
 DB 577 GGTGAGACGTGATGAAAGACCCCTGTAGGAAACACACCAACTGACACTGCTGGGCTC 636
 QY 451 GCCCTCATGTGCGAGGCTTCTCTCCATGACACCTGTGACACAGCTGCA 502
 DB 637 CTGCTAATTCAGAAAGAAATGCAACACATGACATGTATGTTCGGAAACA 688

RESULT 9
 US-08-974-186-1
 Sequence 1, Application US/08974186
 Patent No. 6284740

GENERAL INFORMATION:
 APPLICANT: Boyle, William J.
 APPLICANT: Lacey, David L.
 APPLICANT: Calzone, Frank J.
 APPLICANT: Chang, Ming-Shi
 TITLE OF INVENTION: OSTEOPROTEGERIN
 NUMBER OF SEQUENCES: 53
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Amgen Inc.
 STREET: 1840 Dehavilland Drive
 CITY: Thousand Oaks
 STATE: California
 COUNTRY: USA
 ZIP: 91320-1789
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30

APPLICANT: Boyle, William
APPLICANT: Lacey, David
APPLICANT: Calzone, Frank
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: Osteoprotegerin
FILE REFERENCE: A-378CIP
CURRENT APPLICATION NUMBER: US/08/706,945D
CURRENT FILING DATE: 1996-09-03
PRIOR APPLICATION NUMBER: 08/577,788
PRIOR FILING DATE: 1995-12-22
NUMBER OF SEQ ID NOS: 145
SOFTWARE: PatentIn version 3.1
SEQ ID NO 123
LENGTH: 2432
TYPE: DNA
ORGANISM: Rattus rattus
FEATURE:
NAME/KEY: CDS
LOCATION: (124)..(1326)
OTHER INFORMATION:
US-08-706-945D-123

Query Match 13.8%; Score 112; DB 4; Length 2432;
Best Local Similarity 52.3%; Pred. No. 2.8e-14;
Matches 247; Conservative 0; Mismatches 225; Indels 0; Gaps 0;

QY 31 GACGACAGAGACAGGAGGAGCGCTGTGTGCGCCAGTGCACCCCGACCTTTGTGACG 90
DB 217 GACCCAGAAACCGAGCTCAGCTTTGTGTACAAATGTGCTCTGTGACCTTACTTAAAA 276
QY 91 CGGCGGTGCGCGGAGACAGACCCCGACGCTGTGCGCCGTGTCCACCGCCCACTACAG 150
DB 277 CAGCAGCTGACAGTACAGAGAGAGACACTGTGTGCTTCCCTGACCTACTTATATACA 336
QY 151 CAGTTCTGGAACCTACCTGAGCGCTGCGCTACTGCAACTCTCTCGGGAGCGGTGAG 210
DB 337 GAGAGCTGGACACAGATGTGATGTGTACTGACGCGCCCGGTGCAAGAACTGACG 396
QY 211 GAGAGGACAGGAGCTTGCACGCGACCAACCGTGTGCGCTGCGCGTGCAGACCGGCTTC 270
DB 397 ACCGTGAAGAGAGTGAACCCGACCAACCGAGTGTGCGAATGTGAGAAAGGCGC 456
QY 271 TTGCGCAGCGCTGTGTTCTCTGTGAGACGCAATCGTCCACCTGTGCGCGGTGATT 330
DB 457 TACCTGAGCTGCAATCTCTGTGAAGACCGAGCTGTCCCGACGCTTGGGTGCTG 516
QY 331 GCGCGGAGACCCCGACGACGACGAGTGCAGCGCGTGCAGCGCGCCCGACCTTCTCA 390
DB 517 CAGGCTGGAGACCCGACGACGACGAGTGTGCAAAAGATGTCCGATGGGTTCTTCTCA 576
QY 391 GCCAGAGCTCCAGCTGAGAGCACTGCGACCCCGACCGCAACTGACGCGCTTGGGCTG 450
DB 577 GGTGAGAGCTGATGAAAGACCTGTGAGAAACACACCACTGCACTTGGGCTC 636
QY 451 GCCCTCAATGTGCGAGCTCTTCTCCATGACACCTGTGACACCACTGCA 502
DB 637 CTGCTAATTCAGAAAGAAATGCAACATGACATATGTTCCGGAACA 688

RESULT 12
US-08-974-022-3
Sequence 3, Application US/08974022
Patent No. 6015938
GENERAL INFORMATION:
APPLICANT: Boyle, William J.
APPLICANT: Lacey, David L.
APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: OSTEOPROTEGERIN
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STREET: 1840 Dehavilland Drive

CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,022
FILING DATE: 12-DEC-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/577,788
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-378
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1324 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 90..1292
US-08-974-022-3

Query Match 13.6%; Score 110.4; DB 3; Length 1324;
Best Local Similarity 52.1%; Pred. No. 5.5e-14;
Matches 246; Conservative 0; Mismatches 226; Indels 0; Gaps 0;

QY 31 GACGACAGAGACAGGAGGAGCGCTGTGTGCGCCAGTGCACCCCGACCTTTGTGACG 90
DB 183 GACCCAGAAACGTGATCATGCTCTGTGTGACAAATGTGCTCTGTGACCTTACTTAAAA 242
QY 91 CGGCGGTGCGCGGAGACAGACCCCGACGCTGTGCGCCGTGTCCACCGCCCACTACAG 150
DB 243 CAGCAGCTGACAGTGAAGAGAGAAACATGTGTGCTTCCCTGACCTCTTATACG 302
QY 151 CAGTTCTGGAACCTACCTGAGCGCTGCGCTACTGCAAGTCTCTGCGGGAGCGGTGAG 210
DB 303 GAGAGCTGGACACAGTGTGATGTGTATTGACGCCAGTGTGACAGAACTGACG 362
QY 211 GAGAGGACAGGAGCTTGCACGCGACCAACACCGTGTGCGCTGCGCGTGCAGACCGCTTC 270
DB 363 TCGGTGAAGAGAGAGTGAACCGCACCCACCAACCGAGTGTGATGTGAGAAAGGCGCT 422
QY 271 TTGCGCAGCGCTGTGTTCTCTGTGAGACGCAATCGTGTCCACCTGTGCGCGGTGATT 330
DB 423 TACCTGAGATTCGAATCTCTGTGAAGACCGGAGCTGTCCCGGAGCTCCGGGTG 482
QY 331 GCGCGGAGACCCCGACGACGACGAGTGCAGCGCGTGCAGCGCGCCCGACCACTTCTCA 390
DB 483 CAGCTGGAACCCCGACGACGACGAGTGTGCAAAAGATGTCCAGATGGGTTCTTCTCA 542
QY 391 GCCAGAGCTCCAGCTGAGAGCACTGCGACCCCGACCGCAACTGACGCGCGCTTGGGCTG 450
DB 543 GGTGAGAGCTTATGAAAGACCTGTATTAACACACCACTGCACTTGGGCTC 602
QY 451 GCCCTCAATGTGCGAGCTCTTCTCCATGACACCTGTGACCACTGCA 502
DB 603 CTGCTAATTCAGAAAGAAATGCAACATGACATGACATGTTCCGGAACA 654

RESULT 13
US-08-795-445A-3
Sequence 3, Application US/08795445A
Patent No. 6284485
GENERAL INFORMATION:

APPLICANT: Boyle, William J.
APPLICANT: Lacey, David L.
APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: OSTEOPROTEGERIN
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STREET: 1840 DeHavilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320-1789
COMPUTER READABLE FORM: disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,445A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/577,788
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-378
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1324 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
FEATURE:
NAME/KEY: CDS
LOCATION: 90..1292
US-08-795-445A-3

Query Match 13.6%; Score 110.4; DB 4; Length 1324;
Best Local Similarity 52.1%; Pred. No. 5.5e-14;
Matches 246; Conservative 0; Mismatches 226; Indels 0; Gaps 0;

QY 31 GACGACAGACAGGGGAGCGCTGGTGGCGCCAGTGCCTCCCGCCAGGACACTTTGTGCAG 90
DB 183 GACCCAGAACTGGTTCATCAGCTCTGTGTGACAAATGTCTCTGGCACCTACCTAAAA 242

QY 91 CGGCCGTGCCCGGAGACAGCCCGACGACGTGGCGCCGCTGTCCACCGCCACTACAG 150
DB 243 CAGCACTGCACAGTGAAGGAGACATTTGTGTCTCCCTTGCCCTGACCACTCTTATACG 302

QY 151 CAGTTCTGGAATACCTGAGCGGTGCGCTACTGCAACGCTCTCTCGGGGAGCGTGAG 210
DB 363 TCCGTGAAGCAGGAGTGAACCGACCCACACCGAGTGTGTGAGTGTGAGGAGGGCGT 422

QY 271 TTCGGCAGCGTGGTTCTCTGTTGGAGCAGCATCGTGTCCACTCTGTGCGCGGTGATT 330
DB 423 TACCTGGAGATCGAATCTGCTTGAAGCAGCGGAGCTGTCCCGGGCTCCGGGGTGGTG 482

QY 331 GCCCGGACCCCGGACAGACCGGAGTGCAGCGCTGCCCGCCAGGACCTTCTCA 390
DB 483 CAAGCTGGAACCCCGAGCGAAACACAGTTTGCAGATGAGTTCTTCTCA 542

QY 391 GCCAGCACTCCAGCTCAGAGCAGTGCAGCGCCCGCCAGCACTGCAGCGCCCTGGCGCTG 450
DB 543 GGTGAGACTTCATCGAAGACCCCTGTATATAACACACAGCACTGCAGCACATTTGGCCTC 602

QY 451 GCCCTCAATGTGCCAGGCTCTCTCTCCCATGACACCTCTGTGCACAGCTGCA 502

DB 603 CTGCTAATTCAGAAAGGAATGCAACACATGACAACTGTGTTCGGAACA 654

RESULT 14
US-08-795-447A-3
Sequence 3, Application US/08/795447A
Patent No. 6254728
GENERAL INFORMATION:
APPLICANT: Boyle, William J.
APPLICANT: Lacey, David L.
APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: Osteoprotegerin
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STREET: One Amgen Center Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91362-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,447A
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-378D2
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1324 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
FEATURE:
NAME/KEY: CDS
LOCATION: 90..1292
US-08-795-447A-3

Query Match 13.6%; Score 110.4; DB 4; Length 1324;
Best Local Similarity 52.1%; Pred. No. 5.5e-14;
Matches 246; Conservative 0; Mismatches 226; Indels 0; Gaps 0;

QY 31 GACGACAGACAGGGGAGCGGTGGTGGCGCCAGTGCCTCCCGCCAGGACACTTTGTGCAG 90
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QY 211 GAGGAGCAGCGGTGGCCAGCCACCCACCGTGCCTGCGCGCTGCCGACCGGCTTC 270
DB 363 TCCGTGAAGCAGGAGTGAACCGACCCACACCGAGTGTGTGAGTGTGAGGAGGGCGT 422

QY 271 TTCGGCAGCGTGGTTCTCTGTTGGAGCAGCATCGTGTCCACTCTGTGCGCGGTGATT 330
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QY 331 GCCCGGACCCCGGACAGACCGGAGTGCAGCGCTGCCCGCCAGGACCTTCTCA 390
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RESULT 15

US-08-974-186-3
Sequence 3, Application US/08974186
Patent No. 6284740
GENERAL INFORMATION:
APPLICANT: Boyle, William J.
APPLICANT: Lacey, David L.
APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: OSTEOPROTEGERIN
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STREET: 1840 Denavilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,186
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/577,788
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-378
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1324 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 90..1292
US-08-974-186-3

Query Match 13.6%; Score 110.4; DB 4; Length 1324;
Best local similarity 52.1%; Pred. No. 5.5e-14;
Matches 246; Conservative 0; Mismatches 226; Indels 0; Gaps 0;

QY 31 GACGACAGACAGAGGAGCGCTGTGTGCGCCAGTGCACCCCGAGCACCCTTTGTGACG 90
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DB 363 TCCGTGAAGAGAGTGCACACCGCACCCACCAACGAGTGTGTGAGTGTGAGAAAGGCGT 422
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QY 331 GCCCGGGGCAACCCCAAGCAGAAACAGCAGTGCAGCGCTGCCCCCGGACACTTCTCA 390
DB 483 CAAGCTGGAACCCCAAGAGGAAACAGTTTGCAGAAAATGTCAAGATGGGTTCTTCTCA 542
QY 391 GCCAGCAGCTCCAGCTCAGAGCAGTGCAGCCCAACCGCAACTGCACGCGCTGGCCTG 450
DB 543 GGTGAGACTTCATCGAAGAACACCCCTGTATTAACACACAGAACTGCAGCAATTTGGCCTC 602
QY 451 GCCCTCAATGTGCAGGCTCTTCTCCCATGACACCTGTGCACCGCTGCA 502
DB 603 CTGCTAATTGAGAAAGAAATGCAACATGACACGCTGTCTCGGAAACA 654

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Job time : 59 secs

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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: January 6, 2003, 13:55:36 ; Search time 58 Seconds
(without alignments)
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Title: US-09-936-024-2

Perfect score: 813

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 381593 seqs, 216252194 residues

Total number of hits satisfying chosen parameters: 763186

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 100%

Listing first 45 summaries

Database :

Published Applications NA:*

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- 14: /cgn2_6/prodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	813	100.0	1077	10	US-09-935-727-1	Sequence 1, Appli
2	813	100.0	1114	10	US-09-896-096A-2	Sequence 2, Appli
3	813	100.0	1114	10	US-09-894-924-2	Sequence 2, Appli
4	813	100.0	1347	10	US-09-877-156-18	Sequence 18, Appli
5	809.4	99.6	1137	10	US-09-840-795-1	Sequence 7, Appli
6	533.4	65.6	1859	10	US-09-877-156-19	Sequence 19, Appli
7	515.4	63.4	903	10	US-09-935-727-32	Sequence 32, Appli
8	473.4	58.2	491	10	US-09-896-096A-3	Sequence 3, Appli
9	473.4	58.2	491	10	US-09-894-924-3	Sequence 3, Appli
10	459	56.5	459	10	US-09-877-156-7	Sequence 7, Appli
11	392.2	48.2	1550	10	US-09-935-727-33	Sequence 33, Appli
12	387.4	47.7	1667	10	US-09-935-727-3	Sequence 3, Appli
13	387	47.6	1796	10	US-09-935-727-28	Sequence 28, Appli
14	245.2	30.2	271	10	US-09-896-096A-5	Sequence 5, Appli
15	245.2	30.2	271	10	US-09-894-924-5	Sequence 5, Appli
16	242.2	29.8	283	10	US-09-896-096A-10	Sequence 10, Appli
17	242.2	29.8	283	10	US-09-894-924-10	Sequence 10, Appli
18	220.8	27.2	499	10	US-09-935-727-17	Sequence 17, Appli
19	218.8	26.9	226	10	US-09-896-096A-9	Sequence 9, Appli

20	218.8	26.9	226	10	US-09-894-924-9	Sequence 9, Appli
21	200	24.6	201	10	US-09-896-096A-6	Sequence 6, Appli
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23	194.2	23.9	199	10	US-09-896-096A-8	Sequence 8, Appli
24	194.2	23.9	199	10	US-09-894-924-8	Sequence 8, Appli
25	183	22.5	233	9	US-09-292-758-141	Sequence 141, Appli
26	179	22.0	191	10	US-09-935-727-18	Sequence 18, Appli
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31	103	12.7	819	10	US-09-062-113-96	Sequence 96, Appli
32	103	12.7	966	10	US-09-062-113-101	Sequence 101, App
33	103	12.7	981	10	US-09-062-113-92	Sequence 92, Appli
34	103	12.7	984	10	US-09-062-113-93	Sequence 93, Appli
35	103	12.7	1056	10	US-09-062-113-95	Sequence 95, Appli
36	103	12.7	1089	10	US-09-062-113-100	Sequence 100, App
37	103	12.7	1182	10	US-09-062-113-94	Sequence 94, Appli
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45	103	12.7	1206	10	US-09-062-113-87	Sequence 87, Appli

ALIGNMENTS

RESULT 1
US-09-935-727-1
Sequence 1, Application US/09935727
Patent No. US20020150583A1
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Tumor Necrosis Factor Receptors 6 Alpha and 6 Beta
FILE REFERENCE: P4454P2
CURRENT APPLICATION NUMBER: US/09/935,727
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: 60/303,224
PRIOR FILING DATE: 2001-07-06
PRIOR APPLICATION NUMBER: 60/252,131
PRIOR FILING DATE: 2000-11-21
PRIOR APPLICATION NUMBER: 60/227,598
PRIOR FILING DATE: 2000-08-25
PRIOR APPLICATION NUMBER: 09/518,931
PRIOR FILING DATE: 2000-03-03
PRIOR APPLICATION NUMBER: 60/168,235
PRIOR FILING DATE: 1999-12-01
PRIOR APPLICATION NUMBER: 60/146,371
PRIOR FILING DATE: 1999-08-02
PRIOR APPLICATION NUMBER: 60/131,964
PRIOR FILING DATE: 1999-04-30
PRIOR APPLICATION NUMBER: 60/131,270
PRIOR FILING DATE: 1999-04-27
PRIOR APPLICATION NUMBER: 60/124,092
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/121,774
PRIOR FILING DATE: 1999-03-04
PRIOR APPLICATION NUMBER: 09/006,352
PRIOR FILING DATE: 1998-01-13
PRIOR APPLICATION NUMBER: 60/035,496
PRIOR FILING DATE: 1997-01-14
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 1077
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS

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; LOCATION: (25)...(924)
US-09-935-727-1

Query Match      100.0%; Score 813; DB 10; Length 1077;
Best Local Similarity 100.0%; Pred. No. 7.8e-162;
Matches 813; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGCAGAAACACCCACCTACCCCTGGCGGAGCGAGACAGAGAGAGCGGCTGGTGTC 60
DB 112 GTGGCAGAAACACCCACCTACCCCTGGCGGAGCGAGACAGAGAGAGCGGCTGGTGTC 171

QY 61 GCCAGTGCCCGCCAGCAGCTTTGTGACGCGCGCGTGGCGAGACAGCCACGACG 120
DB 172 GCCAGTGCCCGCCAGCAGCTTTGTGACGCGCGCGTGGCGAGACAGCCACGACG 231

QY 121 TGTGGCCCGTGTCCACCGCGCCACTACACGAGTTCTGGAACTACCTGGAGCGCTGCCG 180
DB 232 TGTGGCCCGTGTCCACCGCGCCACTACACGAGTTCTGGAACTACCTGGAGCGCTGCCG 291

QY 181 TACTGCAACGCTCTCTGCGGGAGCGTGGAGGAGGACAGGGCTTGCACGCCACCCAC 240
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QY 241 AACCGTGCCTGCGCTGCGCGACCGGCTTCTGCGCAGCGTGGTTTCTGTTGGAGCAC 300
DB 352 AACCGTGCCTGCGCTGCGCGACCGGCTTCTGCGCAGCGTGGTTTCTGTTGGAGCAC 411

QY 301 GCATCGTGTCCACCTGTGCGCGGTGATTGGCCCGGGCACCCCGAGCCAGAAACGCGAG 360
DB 412 GCATCGTGTCCACCTGTGCGGGGTGATTGGCCCGGGCACCCCGAGCCAGAAACGCGAG 471

QY 361 TGCAGCGCTGCGCGCCCGCAGGACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 420
DB 472 TGCAGCGCTGCGCGCCCGCAGGACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 531

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QY 481 GACACCTGTGCACCACTGCAGCTGGCTTCCCTCTCAGCACCAAGGTTACGAGGAGCTGAG 540
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RESULT 2

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US-09-896-096A-2
; Sequence 2, Application US/09896096A
; Patent No. US20020061559A1
; GENERAL INFORMATION:
; APPLICANT: ASHKENAZI, AVI J
; APPLICANT: BOTSTEIN, DAVID
; APPLICANT: DODGE, KELLY H.
; APPLICANT: GURNEY, AUSTIN L.
```

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; APPLICANT: KIM, KYUNG JIN
; APPLICANT: LAWRENCE, DAVID A.
; APPLICANT: FITTI, ROBERT
; APPLICANT: ROY, MARGARET A
; APPLICANT: TUMAS, DANIEL B
; APPLICANT: WOOD, WILLIAM I.
; TITLE OF INVENTION: DcE3 Polypeptide, A TNFR Homolog
; FILE REFERENCE: P1134R2 REVISED
; CURRENT APPLICATION NUMBER: US/09/896,096A
; PRIOR FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US 09/157,289
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: US 60/059,288
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: US 60/094,640
; PRIOR FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 18
; SEQ ID NO 2
; LENGTH: 1114
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: Unsure
; LOCATION: 1090
; OTHER INFORMATION: Unknown base
US-09-896-096A-2

Query Match      100.0%; Score 813; DB 10; Length 1114;
Best Local Similarity 100.0%; Pred. No. 7.8e-162;
Matches 813; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGCAGAAACACCCACCTACCCCTGGCGGAGCGAGACAGAGAGAGCGGCTGGTGTC 60
DB 188 GTGGCAGAAACACCCACCTACCCCTGGCGGAGCGAGACAGAGAGAGCGGCTGGTGTC 247

QY 61 GCCAGTGCCCGCCAGCAGCTTTGTGACGCGCGCTGGCGGACAGAGAGAGCGGCTGGTGTC 120
DB 248 GCCAGTGCCCGCCAGCAGCTTTGTGACGCGCGCTGGCGGACAGAGAGAGCGGCTGGTGTC 307

QY 121 TGTGGCCCGTGTCCACCGCGCCACTACACGAGTTCTGGAACTACCTGGAGCGCTGCCGC 180
DB 308 TGTGGCCCGTGTCCACCGCGCCACTACACGAGTTCTGGAACTACCTGGAGCGCTGCCGC 367

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RESULT 3
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; Sequence 2, Application US/09894924
; Patent No. US20020065210A1
; GENERAL INFORMATION:
; APPLICANT: ASHKENAZI, AVI J
; APPLICANT: BOTSSTEIN, DAVID
; APPLICANT: DODGE, KELLY H.
; APPLICANT: GURNEY, AUSTIN L.
; APPLICANT: KIM, KYUNG JIN
; APPLICANT: LAWRENCE, DAVID A.
; APPLICANT: PITTI, ROBERT
; APPLICANT: ROY, MARGARET A
; APPLICANT: TOMAS, DANIEL B
; APPLICANT: WOOD, WILLIAM I.
; TITLE OF INVENTION: DCR3 Polypeptide, A TNFR Homolog
; FILE REFERENCE: P1134R2 REVISED
; CURRENT APPLICATION NUMBER: US/09/894,924
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US 09/157,289
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: US 60/059,288
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: US 60/094,640
; PRIOR FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 18
; SEQ ID NO 2
; LENGTH: 1114
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: Unsure
; LOCATION: 1090
; OTHER INFORMATION: Unknown base
US-09-894-924-2

Query Match 100.0%; Score 813; DB 10; Length 1114;
Best Local Similarity 100.0%; Pred. No. 7,8e-162;
Matches 813; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGCAGAAACACCACCTTACCTGCGGGAGCGCAGAGACAGGGGAGCGGCTGTGTGC 60
Db 188 GTGGCAGAAACACCACCTTACCTGCGGGAGCGCAGAGACAGGGGAGCGGCTGTGTGC 247
Qy 61 GCCCAGTGCCCGCCAGGACCTTGTGTGAGCGGCGCTGCCCGCAGACAGCCCGACGACG 120
Db 248 GCCCAGTGCCCGCCAGGACCTTGTGTGAGCGGCGCTGCCCGCAGACAGCCCGACGACG 307
Qy 121 TGTGGCCCGTGTCCACCGCGCCTACACGAGTTCTGGAATCTAGAGCGCTGCCGC 180
Db 308 TGTGGCCCGTGTCCACCGCGCCTACACGAGTTCTGGAATCTAGAGCGCTGCCGC 367
Qy 181 TACTGCAACGCTCTGTGGGGAGGTGAGGAGGAGCGGCGCTTGCAGCCACCCAC 240
Db 368 TACTGCAACGCTCTGTGGGGAGGTGAGGAGGAGCGGCGCTTGCAGCCACCCAC 427
Qy 241 AACCGTCTGCTGCGCGCAGCGGCTTCTTCCGCGACGCTGTGTTCTGCTTGAAGCAC 300

Db 428 AACCGTCTGCTGCGCGCAGCGGCTTCTTTCGCGCAGCGCTGTCTTGTGTCAGAC 487
Qy 301 GCATCGTGTCCACCTGATGCGGCGGTGATGTCGCCGGGACCCCGACGAGCAACAGCAG 360
Db 488 GCATCGTGTCCACCTGATGCGGCGGTGATGTCGCCGGGACCCCGACGAGCAACAGCAG 547
Qy 361 TGCACAGCGTGCCTCCCGAGGACCTTCTCAGCAGCAGAGCTTCAGAGCAGTGCAG 420
Db 548 TGCACAGCGTGCCTCCCGAGGACCTTCTCAGCAGCAGAGCTTCAGAGCAGTGCAG 607
Qy 421 CCCACCGCAACTGCAAGGCGCTGCGGCTGCGGCTCAATGTGCAAGCTTCTCCCAT 480
Db 608 CCCACCGCAACTGCAAGGCGCTGCGGCTGCGGCTCAATGTGCAAGCTTCTCCCAT 667
Qy 481 GACACCTGTGCAACAGCTGCTGCTCCCTCAGCAGCAGGAGTACAGGAGCTGAG 540
Db 668 GACACCTGTGCAACAGCTGCTGCTCCCTCAGCAGCAGGAGTACAGGAGCTGAG 727
Qy 541 GAGTGTAGCGTGCCTGATGCACTTGTGCTTTCAGGACATCTTCATCAAGAGCTG 600
Db 728 GAGTGTAGCGTGCCTGATGCACTTGTGCTTTCAGGACATCTTCATCAAGAGCTG 787
Qy 601 CAGCGGCTGCTGCAAGGCGCTGCAAGGCGCGGAGGCGCTGCGGCTCCAGACCAAGGCGGCG 660
Db 788 CAGCGGCTGCTGCAAGGCGCTGCAAGGCGCGGAGGCGCTGCGGCTCCAGACCAAGGCGGCG 847
Qy 661 CGCGCGCTTGTGACGCTGAAGCTGCGGCGGCTCAAGAGCTCTTGGGGGCGCAGGAC 720
Db 848 CGCGCGCTTGTGACGCTGAAGCTGCGGCGGCTCAAGAGCTCTTGGGGGCGCAGGAC 907
Qy 721 GGGGCGCTGCTGTCAGGCTGCTGTCAGGCGCTGCGGCTGCGCAGAGTCCCGGCTGAG 780
Db 908 GGGGCGCTGCTGTCAGGCTGCTGTCAGGCGCTGCGGCTGCGCAGAGTCCCGGCTGAG 967
Qy 781 CGAGAGCTCTGTCAGGCTCTCTCTCTCTGTCAC 813
Db 968 CGAGAGCTCTGTCAGGCTCTCTCTCTCTGTCAC 1000

RESULT 4
US-09-877-156-18
; Sequence 18, Application US/09877156
; Patent No. US20020055625A1
; GENERAL INFORMATION:
; APPLICANT: Catherine Tribouley
; TITLE OF INVENTION: NEW MEMBERS OF TNF AND TNFR FAMILIES
; FILE REFERENCE: 1408.003/200130.439C1
; CURRENT APPLICATION NUMBER: US/09/877,156
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 09/286,529
; PRIOR FILING DATE: 1998-04-05
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 18
; LENGTH: 1347
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-877-156-18

Query Match 100.0%; Score 813; DB 10; Length 1347;
Best Local Similarity 100.0%; Pred. No. 8e-162;
Matches 813; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGCAGAAACACCACCTTACCTTGGCGGAGCGCAGAGACAGGGGAGCGGCTGTGTGC 60
Db 405 GTGGCAGAAACACCACCTTACCTTGGCGGAGCGCAGAGACAGGGGAGCGGCTGTGTGC 464
Qy 61 GCCCAGTGCCCGCCAGGACCTTGTGTGAGCGGCGCTGCCCGCAGACAGCCCGACGACG 120
Db 465 GCCCAGTGCCCGCCAGGACCTTGTGTGAGCGGCGCTGCCCGCAGACAGCCCGACGACG 524
Qy 121 TGTGGCCCGTGTCCACCGCGCCTACACGAGTTCTGGAATCTAGAGCGCTGCCGC 180

;; TITLE OF INVENTION: NEW MEMBERS OF TNF AND TNFR FAMILIES
;; FILE REFERENCE: 1408.003/200130.439C1
;; CURRENT APPLICATION NUMBER: US/09/877.156
;; CURRENT FILING DATE: 2001-06-08
;; PRIOR APPLICATION NUMBER: US 09/286,529
;; PRIOR FILING DATE: 1998-04-05
;; NUMBER OF SEQ ID NOS: 25
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO: 19
;; LENGTH: 1859
;; TYPE: DNA
;; ORGANISM: Homo sapien
US-09-877-156-19

Query Match 65.6%; Score 533.4; DB 10; Length 1859;
Best Local Similarity 98.9%; Pred. No. 2,6e-103;
Matches 537; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 GTGGGAGAAACACCCACCTTACCCCTGGCGGAGACGACAGACAGGAGGAGCGGCTGTGTGC 60
DB 165 GTGGGAGAAACACCCACCTTACCCCTGGCGGAGACGACAGACAGGAGGAGCGGCTGTGTGC 224
QY 61 GCGCAGTGGCCCCCGGAGCAGCTTTGTGAGAGGCGGCTGCGCCGAGACAGCCCAAGCAGC 120
DB 225 GCGCAGTGGCCCCCGGAGCAGCTTTGTGAGAGGCGGCTGCGCCGAGACAGCCCAAGCAGC 284
QY 121 TGTGGCCCGTGTCCACCGCGGACCTACACGAGTTCTGGAATCTAGAGAGCGTGCAGC 180
DB 285 TGTGGCCCGTGTCCACCGCGGACCTACACGAGTTCTGGAATCTAGAGAGCGTGCAGC 344
QY 181 TACTGCAACGTCTCTCTGCGGGAGCGTGAAGAGAGAGGACGCGGCTTGCCAGCCACCAC 240
DB 345 TACTGCAACGTCTCTCTGCGGGAGCGTGAAGAGAGAGGACGCGGCTTGCCAGCCACCAC 404
QY 241 AACGTCGCTGCGGCTGCGGACCGGCTTCTTGGCGACGCTGTTTCTGTTGGAGCAC 300
DB 405 AACGTCGCTGCGGCTGCGGACCGGCTTCTTGGCGACGCTGTTTCTGTTGGAGCAC 464
QY 301 GCATGCTGTCCACCTGGTGGCGGCGGTGATTGCGCCGGGACACCCCGAGCAGAACAGCAG 360
DB 465 GCATGCTGTCCACCTGGTGGCGGCGGTGATTGCGCCGGGACACCCCGAGCAGAACAGCAG 524
QY 361 TGCCAGCGTGGCCCCCGGAGCAGCTTCTCAAGCAGACAGCTTCAAGTGAAGTGCAG 420
DB 525 TGCCAGCGTGGCCCCCGGAGCAGCTTCTCAAGCAGACAGCTTCAAGTGAAGTGCAG 584
QY 421 CCCCACCGCACTGCAAGCGGCTGCGGCTGCGCTCAATGTGCCAGGCTTCTTCCCAT 480
DB 585 CCCCACCGCACTGCAAGCGGCTGCGGCTGCGCTCAATGTGCCAGGCTTCTTCCCAT 644
QY 481 GACACCGTGTGACAGCTGACAGTGTGCTCCCTCAGACACAGGATACAGAGAGTGCAG 540
DB 645 GACACCGTGTGACAGCTGACAGTGTGCTCCCTCAGACACAGGATACAGAGAGTGCAG 704
QY 541 GAG 543
DB 705 GAG 707

RESULT 7
US-09-935-727-32
; Sequence 32, Application US/09935727
; Patent No. US20020150583A1
; GENERAL INFORMATION:

;; APPLICANT: Human Genome Sciences, Inc.
;; TITLE OF INVENTION: Tumor Necrosis Factor Receptors 6 Alpha and 6 Beta
;; FILE REFERENCE: PF454P2
;; CURRENT APPLICATION NUMBER: US/09/935.727
;; CURRENT FILING DATE: 2001-08-24
;; PRIOR APPLICATION NUMBER: 60/303,224
;; PRIOR FILING DATE: 2001-07-06
;; PRIOR APPLICATION NUMBER: 60/252,131
;; PRIOR FILING DATE: 2000-11-21

;; PRIOR APPLICATION NUMBER: 60/227,598
;; PRIOR FILING DATE: 2000-08-25
;; PRIOR APPLICATION NUMBER: 09/518,931
;; PRIOR FILING DATE: 2000-03-03
;; PRIOR APPLICATION NUMBER: 60/168,235
;; PRIOR FILING DATE: 1999-12-01
;; PRIOR APPLICATION NUMBER: 60/146,371
;; PRIOR FILING DATE: 1999-08-02
;; PRIOR APPLICATION NUMBER: 60/131,964
;; PRIOR FILING DATE: 1999-04-30
;; PRIOR APPLICATION NUMBER: 60/131,270
;; PRIOR FILING DATE: 1999-04-27
;; PRIOR APPLICATION NUMBER: 60/124,092
;; PRIOR FILING DATE: 1999-03-12
;; PRIOR APPLICATION NUMBER: 60/121,774
;; PRIOR FILING DATE: 1999-03-04
;; PRIOR APPLICATION NUMBER: 09/006,352
;; PRIOR FILING DATE: 1998-01-13
;; PRIOR APPLICATION NUMBER: 60/035,496
;; PRIOR FILING DATE: 1997-01-14
;; NUMBER OF SEQ ID NOS: 42
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO: 32
;; LENGTH: 903
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Mammalian synthetic TNFR-6 alpha
US-09-935-727-32

Query Match 63.4%; Score 515.4; DB 10; Length 903;
Best Local Similarity 77.1%; Pred. No. 1.4e-99;
Matches 627; Conservative 0; Mismatches 186; Indels 0; Gaps 0;

QY 1 GTGGGAGAAACACCCACCTTACCCCTGGCGGAGACGACAGACAGGAGGAGCGGCTGTGTGC 60
DB 88 GTGGGAGAAACACCCACCTTACCCCTGGCGGAGACGACAGACAGGAGGAGCGGCTGTGTGC 147
QY 61 GCGCAGTGGCCCCCGGAGCAGCTTTGTGAGAGGCGGCTGCGCCGAGACAGCCCAAGCAGC 120
DB 148 GCGCAGTGGCCCCCGGAGCAGCTTTGTGAGAGGCGGCTGCGCCGAGACAGCCCAAGCAGC 207
QY 121 TGTGGCCCGTGTCCACCGCGGACCTTGTGAGAGGCGGCTGCGCCGAGACAGCCCAAGCAGC 180
DB 208 TGTGGCCCGTGTCCACCGCGGACCTTGTGAGAGGCGGCTGCGCCGAGACAGCCCAAGCAGC 267
QY 181 TACTGCAACGTCTCTCTGCGGGAGCGTGAAGAGAGAGGACGCGGCTTGCCAGCCACCAC 240
DB 268 TACTGCAACGTCTCTCTGCGGGAGCGTGAAGAGAGAGAGGACGCGGCTTGCCAGCCACCAC 327
QY 241 AACCGTGGCTGGCGGCGGACCGGCTTCTTGGCGAGCGTGTTCCTGTGAGACAC 300
DB 328 AACCGTGGCTGGCGGCGGACCGGCTTCTTGGCGAGCGTGTTCCTGTGAGACAC 387
QY 301 GCATGCTGTCCACCTGGTGGCGGCGGTGATTGCGCCGGGACACCCCGAGCAGAACAGCAG 360
DB 388 GCATGCTGTCCACCTGGTGGCGGCGGTGATTGCGCCGGGACACCCCGAGCAGAACAGCAG 447
QY 361 TGCCAGCGTGGCCCCCGGAGCAGCTTCTCAAGCAGACAGCTTCAAGTGAAGTGCAG 420
DB 448 TGCCAGCGTGGCCCCCGGAGCAGCTTCTCAAGCAGACAGCTTCAAGTGAAGTGCAG 507
QY 421 CCCCACCGCACTGCAAGCGGCTGCGGCTGCGCTCAATGTGCCAGGCTTCTTCCCAT 480
DB 508 CCCCACCGCACTGCAAGCGGCTGCGGCTGCGCTCAATGTGCCAGGCTTCTTCCCAT 567
QY 481 GACACCGTGTGACAGCTGACAGTGTGCTCCCTCAGACACAGGATACAGAGAGTGCAG 540
DB 568 GACACCGTGTGACAGCTGACAGTGTGCTCCCTCAGACACAGGATACAGAGAGTGCAG 627
QY 541 GAGTGTGAGGCGGCTGACAGCTTGTGAGGCTTTCAGAGACATTCATCAAGAGCTGC 600
DB 628 GAGTGTGAGGCGGCTGACAGCTTGTGAGGCTTTCAGAGACATTCATCAAGAGCTGC 687

QY 601 CAGCGGTGCTGACGGCCCTCGAGGCCCGAGGGCTGGGGTCCGACACCAAGGGCGGC 660
|||
Db 688 CAACGCCTGCTGCAAGCTCTGGAAAGCTCTCGAGGGCTGGGGTCCACACCAAGGGCTGGC 747
|||
QY 661 CGCGCGCCCTTGGACGTGAAGCTCGCTCGGGCTCACGGAGCTCTCTGGGGGCGCAGGAC 720
|||
Db 748 AGGCTGCACTGCNACTGAAGCTTCGGCAGAGGCTCACTGAACTCTCTGGAGCTCAAGAT 807
|||
QY 721 GGGCGCTGCTGGTGGCGCTGCTGACGGCTGCGCGCTGCGCAGGATGCCCGGGCTGGAG 780
|||
Db 808 GGAGCTCTGCTGGTGGCTGCTGCAAGCTCTGAGGGTGGCAAGGATGCCCTGGACTGGAG 867
|||
QY 781 CGGAGCTGCTGCTGAGCGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 813
|||
Db 868 CGCTCTGAGGGAACGCTTCT 900
|||

RESULT 8

US-09-896-096A-3

; Sequence 3, Application US/09896096A

; Patent No. US20020061559A1

; GENERAL INFORMATION:

; APPLICANT: ASHKENAZI, AVI J

; APPLICANT: BOTSTEIN, DAVID

; APPLICANT: DODGE, KELLY H.

; APPLICANT: GURNEY, AUSTIN L.

; APPLICANT: KIM, KYUNG JIN

; APPLICANT: LAWRENCE, DAVID A.

; APPLICANT: PITTI, ROBERT

; APPLICANT: ROY, MARGARET A.

; APPLICANT: TUMAS, DANIEL B.

; APPLICANT: WOOD, WILLIAM I.

; TITLE OF INVENTION: Dcr3 Polypeptide, A TNFR Homolog

; FILE REFERENCE: P1134R2 REVISED

; CURRENT APPLICATION NUMBER: US/09/896,096A

; CURRENT FILING DATE: 2001-06-28

; PRIOR APPLICATION NUMBER: US 09/157,289

; PRIOR FILING DATE: 1998-09-18

; PRIOR APPLICATION NUMBER: US 60/059,288

; PRIOR FILING DATE: 1997-09-18

; PRIOR APPLICATION NUMBER: US 60/094,640

; PRIOR FILING DATE: 1998-07-30

; NUMBER OF SEQ ID NOS: 18

; SEQ ID NO 3

; LENGTH: 491

; TYPE: DNA

; ORGANISM: Unknown

; FEATURE:

; OTHER INFORMATION: Unknown organism

; NAME/KEY: unsure

; LOCATION: 62, 73, 86, 98

; OTHER INFORMATION: unknown base

US-09-896-096A-3

Query Match

Best Local Similarity 58.2%; Score 473.4; DB 10; Length 491;

Matches 485; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 101 GCCGAGACAGCCCCACGACGTGTGGCCCGTGTCCACCGCGCACTACACGAGTTCTGGA 160
Db 1 GCCGAGACAGCCCCACGACGTGTGGCCCGTGTCCACCGCGCACTACACGAGTTCTGGA 60
|||
QY 161 ACTACCTGGAGCGCTGCGGCTACTGCAACGTCTCTGCGGGAGCGTGAGGAGGACAC 220
Db 61 ANTAACCTGGAGCCTGCGGCTACTGNAACGTCTCTGNGGGAGCGTGAGGAGGACAC 120
|||
QY 221 GGGCTTGCACGCGCACCCACAAACCGTGTGCGGCTGCGCGCACCGGCTTCTTCGCGACG 280
Db 121 GGGCTTGCACGCGCACCCACAAACCGTGTGCGGCTGCGCGCACCGGCTTCTTCGCGACG 180
|||
QY 281 CTGGTTTCTGTTGAGCAGCATCGTGTCCACCTGTGCGGCGTGTGTTGTTGTTGTTGTTGTT 340
|||

Db 181 CTGGTTTCTGTTGAGCAGCATCGTGTCCACCTGTGTGCGGCGTGTGTTGTTGTTGTTGTTG 240
|||
QY 341 CCCCCAGCAGAACACGAGTGGC-AGCGTGTGCCCCCAGGACCTTCTCAGCAGCAGC 399
|||
Db 241 CCCCCAGCAGAACACGAGTGGC-AGCGTGTGCCCCCAGGACCTTCTCAGCAGCAGC 300
|||
QY 400 TCAGCTCAGAGCAGTCCAGGCCCCACCACTGCACGGCCCTGCGGCTTGGCCCTCAAT 459
|||
Db 301 TCAGCTCAGAGCAGTCCAGGCCCCACCACTGCACGGCCCTGCGGCTTGGCCCTCAAT 360
|||
QY 460 GTCCAGGCTCTTCTCTCCCATGACACCTGTGACACGAGTGCACCTGCTTCCCGCTCAGC 519
|||
Db 361 GTCCAGGCTCTTCTCTCCCATGACACCTGTGACACGAGTGCACCTGCTTCCCGCTCAGC 420
|||
QY 520 ACCAGGTTACAGGAGCTGAGGAGTGTGAGCGTGTGCGGTATCGACTTTGTGGCTTTCAG 579
|||
Db 421 ACCAGGTTACAGGAGCTGAGGAGTGTGAGCGTGTGCGGTATCGACTTTGTGGCTTTCAG 480
|||
QY 580 GACATCTCCAT 590
|||
Db 481 GACATCTCCAT 491
|||

RESULT 9

US-09-894-924-3

; Sequence 3, Application US/09894924

; Patent No. US20020065210A1

; GENERAL INFORMATION:

; APPLICANT: ASHKENAZI, AVI J

; APPLICANT: BOTSTEIN, DAVID

; APPLICANT: DODGE, KELLY H.

; APPLICANT: GURNEY, AUSTIN L.

; APPLICANT: KIM, KYUNG JIN

; APPLICANT: LAWRENCE, DAVID A.

; APPLICANT: PITTI, ROBERT

; APPLICANT: ROY, MARGARET A.

; APPLICANT: TUMAS, DANIEL B.

; APPLICANT: WOOD, WILLIAM I.

; TITLE OF INVENTION: Dcr3 Polypeptide, A TNFR Homolog

; FILE REFERENCE: P1134R2 REVISED

; CURRENT APPLICATION NUMBER: US/09/894,924

; CURRENT FILING DATE: 2001-06-28

; PRIOR APPLICATION NUMBER: US 09/157,289

; PRIOR FILING DATE: 1998-09-18

; PRIOR APPLICATION NUMBER: US 60/059,288

; PRIOR FILING DATE: 1997-09-18

; PRIOR APPLICATION NUMBER: US 60/094,640

; PRIOR FILING DATE: 1998-07-30

; NUMBER OF SEQ ID NOS: 18

; SEQ ID NO 3

; LENGTH: 491

; TYPE: DNA

; ORGANISM: Unknown

; FEATURE:

; OTHER INFORMATION: Unknown organism

; NAME/KEY: unsure

; LOCATION: 62, 73, 86, 98

; OTHER INFORMATION: unknown base

US-09-894-924-3

Query Match

Best Local Similarity 58.2%; Score 473.4; DB 10; Length 491;

Matches 485; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 101 GCCGAGACAGCCCCACGACGTGTGGCCCGTGTCCACCGCGCACTACACGAGTTCTGGA 160
Db 1 GCCGAGACAGCCCCACGACGTGTGGCCCGTGTCCACCGCGCACTACACGAGTTCTGGA 60
|||
QY 161 ACTACCTGGAGCGCTGCGGCTACTGCAACGTCTCTGCGGGAGCGTGAGGAGGACAC 220
Db 61 ANTAACCTGGAGCCTGCGGCTACTGNAACGTCTCTGNGGGAGCGTGAGGAGGACAC 120
|||
QY 221 GGGCTTGCACGCGCACCCACCAACCGTGTGCGGCTGCGCGCTGCGCGCTTCTTCGCGACG 280
|||

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Db 121 GGGCTTCCAGCGCACCACCAACCGTCTGCGCTGCGCAGCCGGCTTCTTCGCGCAG 180
Qy 281 CTGATTTCTGCTTGAGAGAGCATGATGTCACCTGGGTCGGGGTATTTGCCCGGGGCA 340
Db 181 CTGATTTCTGCTTGAGAGAGCATGATGTCACCTGGGTCGGGGTATTTGCCCGGGGCA 240
Qy 341 CCCCCCAGCAACACGACGATGCC-AGCCGTGCCCCCAGGACCTTCTGAGCAGCAGC 399
Db 241 CCCCCCAGCAACACGAGTGCCTTACCGTGGCCCCCAGGACCTTCTGAGCAGCAGC 300
Qy 400 TCCAGCTCAAGAGAGTGCACGCCCCACCGCACTGCAAGGCTTGGGCTTGCAT 459
Db 301 TCCAGCTCAAGAGAGTGCACGCCCCACCGCACTGCAAGGCTTGGGCTTGCAT 360
Qy 460 GTGCGAGGCTTCTTCTCCATGACACCTGTCGACGAGCTGCACTGAGCTTCCCTCAGC 519
Db 361 GTGCGAGGCTTCTTCTCCATGACACCTGTCGACGAGCTGCACTGAGCTTCCCTCAGC 420
Qy 520 ACCAGGTTACAGAGAGTGAAGTGTGAGCGTCCATGCACTTGTGGCTTTCAG 579
Db 421 ACCAGGTTACAGAGAGTGAAGTGTGAGCGTCCATGCACTTGTGGCTTTCAG 480
Qy 580 GACATCTCCAT 590
Db 481 GACATCTCCAT 491
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RESULT 10
US-09-877-156-7
; Sequence 7, Application US/09877156
; Patent No. US20020055625A1
; GENERAL INFORMATION:
; APPLICANT: Catherine Tribouley
; TITLE OF INVENTION: NEW MEMBERS OF TNF AND TNFR FAMILIES
; FILE REFERENCE: 1408.003/200130.439C1
; CURRENT APPLICATION NUMBER: US/09/877,156
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 09/286,529
; PRIOR FILING DATE: 1998-04-05
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 459
; TYPE: DNA
; ORGANISM: human
US-09-877-156-7
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Query Match 56.5%; Score 459; DB 10; Length 459;
Best Local Similarity 100.0%; Pred. No. 7,8e-88;
Matches 459; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 166 CTGAGAGCTGCGCTACTGCAACGTCCTCTGCGGGAGCGTGAAGAGAGGACGCGCT 225
Db 1 CTGAGAGCTGCGCTACTGCAACGTCCTCTGCGGGAGCGTGAAGAGAGGACGCGCT 60
Qy 226 TGCAGGCCCAACCAACCGTCTGCGGCAACCGGCTTCTTCCGCGACGCTGCT 285
Db 61 TGCAGGCCCAACCAACCGTCTGCGGCAACCGGCTTCTTCCGCGACGCTGCT 120
Qy 286 TTTGCTTTGAGAGAGCATGTCCTCACTGTCGCGGCTGATTTGCCCGGGACCCCC 345
Db 121 TTTGCTTTGAGAGAGCATGTCCTCACTGTCGCGGCTGATTTGCCCGGGACCCCC 180
Qy 346 AGCCAGAACAGCAGTGCACGCGTGCCTCCCAAGGACCTTCTCAGCAGCTCCAGC 405
Db 181 AGCCAGAACAGCAGTGCACGCGTGCCTCCCAAGGACCTTCTCAGCAGCTCCAGC 240
Qy 406 TCGAGAGAGTGCACGCGGCAACCGCAATGAGCGGCTTGGGCTTGGGCTTCAATGTGCCA 465
Db 241 TCGAGAGAGTGCACGCGGCAACCGCAATGAGCGGCTTGGGCTTGGGCTTCAATGTGCCA 300
Qy 466 GGGCTTCTCTCCATGACACCTGTGCAACGAGTGCAGTGGCTTCCCTCAGACACGAG 525
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Db 301 GGGCTTCTCTCCATGACACCTGTGCAACGAGTGCAGTGCAGCTTCCCTCAGACACGAG 360
Qy 526 GTACCAAGAGCTGAGAGAGTGTAGCGCTGCCGTATGACTTTGTGGCTTCCAGACATC 585
Db 361 GTACCAAGAGCTGAGAGAGTGTAGCGCTGCCGTATGACTTTGTGGCTTCCAGACATC 420
Qy 586 TCCATCAAGAGCTGAGAGCGGCTGTGACAGGCCCTGAG 624
Db 421 TCCATCAAGAGCTGAGAGCGGCTGTGACAGGCCCTGAG 459
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```
RESULT 11
US-09-935-727-33
; Sequence 33, Application US/09935727
; Patent No. US20020150583A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Tumor Necrosis Factor Receptors 6 Alpha and 6 Beta
; FILE REFERENCE: PF454P2
; CURRENT APPLICATION NUMBER: US/09/935,727
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/303,224
; PRIOR FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: 60/252,131
; PRIOR FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: 60/227,598
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: 09/518,931
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: 60/168,235
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: 60/146,371
; PRIOR FILING DATE: 1999-08-02
; PRIOR APPLICATION NUMBER: 60/131,964
; PRIOR FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: 60/131,270
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/124,092
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/121,774
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: 09/006,352
; PRIOR FILING DATE: 1998-01-13
; PRIOR APPLICATION NUMBER: 60/035,496
; PRIOR FILING DATE: 1997-01-14
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 33
; LENGTH: 1550
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Codon optimized TNFR-6 alpha
US-09-935-727-33
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Query Match 48.2%; Score 392.2; DB 10; Length 1550;
Best Local Similarity 67.7%; Pred. No. 8,6e-74;
Matches 550; Conservative 0; Mismatches 263; Indels 0; Gaps 0;
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Qy 1 GTGGCAAGAAACACCAACCTTACCTGCGGGAAGCAGAGACAGGGGAGGGGCTGTGCTG 60
Db 738 GTTGTGAAACACCAACCTTACCTGCGGGAAGATGCTGAATGTTGTAAGACTGTTGT 797
Qy 61 GCCAGTGCCTCCCAAGCACTTTGTGACGCGCCGTGCGCGGAGACAGCCCAAGCAG 120
Db 798 GCTCATGTGTCACCAAGTACTTTGTTTAAAGCATGTGAAGAGATTCTCAACTACT 857
Qy 121 TGTGGCCCGTGTACACCGGCACTACAGCAAGTTTGAATCTAGAGAGGCTGCGCC 180
Db 858 TGTGTGTCATGTTCACCAAGACATTACCTCAATTTGGAATCTAGAGAGATGTACA 917
Qy 181 TACTGAAGGTCTCTGCGGGAGCGTGAAGAGAGCAAGGCGCTTGCACAGCACCAC 240
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GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Tumor Necrosis Factor Receptors 6 Alpha and 6 Beta
FILE REFERENCE: PP454P2
CURRENT APPLICATION NUMBER: US/09/935,727
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: 60/303,224
PRIOR FILING DATE: 2001-07-06
PRIOR APPLICATION NUMBER: 60/252,131
PRIOR FILING DATE: 2000-11-21
PRIOR APPLICATION NUMBER: 60/227,598
PRIOR FILING DATE: 2000-08-25
PRIOR APPLICATION NUMBER: 09/518,931
PRIOR FILING DATE: 2000-03-03
PRIOR APPLICATION NUMBER: 60/168,235
PRIOR FILING DATE: 1999-12-01
PRIOR APPLICATION NUMBER: 60/146,371
PRIOR FILING DATE: 1999-08-02
PRIOR APPLICATION NUMBER: 60/131,964
PRIOR FILING DATE: 1999-04-30
PRIOR APPLICATION NUMBER: 60/131,270
PRIOR FILING DATE: 1999-04-27
PRIOR APPLICATION NUMBER: 60/124,092
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/121,774
PRIOR FILING DATE: 1999-03-04
PRIOR APPLICATION NUMBER: 09/006,352
PRIOR FILING DATE: 1998-01-13
PRIOR APPLICATION NUMBER: 60/035,496
PRIOR FILING DATE: 1997-01-14
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 28
LENGTH: 1796
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: Intron
LOCATION: 425-560
NAME/KEY: Intron
LOCATION: 756-1512
US-09-935-727-28

Query Match          47.6%; Score 387; DB 10; Length 1796;
Best Local Similarity 79.4%; Pred. No. 1,1e-72;
Matches 533; Conservative 1; Mismatches 1; Indels 136; Gaps 1;
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Db 448 GCCCCAGAGGTGTGGCCGAGAGTGTGGAGGGGTCAAGTTGTGATCCAGCCTTGA 507
Qy 337 -----GGCAGCCC 344
Db 508 CCCTGAGCTAGACACACAGTTCCCTGACCCCTGTTCTTCTCTGAGTGCAGGCAACCC 567
Qy 345 CAGCCAGAACAGCAGTGTCCAGCCGTGCCCCCGAGCAGCTTCTGAGCAGCAGCTTCAG 404
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RESULT 14
US-09-896-096A-5
Sequence 5, Application US/09896096A
Patent No. US20020061559A1
GENERAL INFORMATION:
APPLICANT: ASHKENAZI, AVI J
APPLICANT: BOTSTEIN, DAVID
APPLICANT: DODGE, KELLY H.
APPLICANT: GURNEY, AUSTIN L.
APPLICANT: KIM, KYUNG JIN
APPLICANT: LAWRENCE, DAVID A.
APPLICANT: PITT, ROBERT
APPLICANT: ROY, MARGARET A
APPLICANT: TUMAS, DANIEL B
APPLICANT: WOOD, WILLIAM I.
TITLE OF INVENTION: DCR3 Polypeptide, A TNFR Homolog
FILE REFERENCE: P114R2 REVISED
CURRENT APPLICATION NUMBER: US/09/896,096A
CURRENT FILING DATE: 2001-06-28
PRIOR APPLICATION NUMBER: US 09/157,289
PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: US 60/059,288
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: US 60/094,640
PRIOR FILING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 18
SEQ ID NO 5
LENGTH: 271
TYPE: DNA
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Unknown organism
NAME/KEY: unsure
LOCATION: 42, 62, 73, 86, 98, 106, 120, 122, 153, 167, 184, 220, 233
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US-09-896-096A-5

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; APPLICANT: ASHKENAZI, AVI J
; APPLICANT: BOTSTEIN, DAVID
; APPLICANT: DODGE, KELLY H.
; APPLICANT: GURNEY, AUSTIN L.
; APPLICANT: KIM, KYUNG JIN
; APPLICANT: LAWRENCE, DAVID A.
; APPLICANT: PITTI, ROBERT
; APPLICANT: ROY, MARGARET A
; APPLICANT: TUMAS, DANIEL B
; APPLICANT: WOOD, WILLIAM I.
; TITLE OF INVENTION: Dcr3 Polypeptide, A TNFR Homolog
; FILE REFERENCE: P1134R2 REVISED
; CURRENT APPLICATION NUMBER: US/09/894,924
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US 09/157,289
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: US 60/059,288
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: US 60/094,640
; PRIOR FILING DATE: 1998-07-30
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; TYPE: DNA
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; FEATURE:
; OTHER INFORMATION: Unknown organism
; NAME/KEY: unsure
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US-09-894-924-5

Query Match 30.2%; Score 245.2; DB 10; Length 271;
Best Local Similarity 92.3%; Pred. No. 3.8e-43;
Matches 250; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
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GenCore version 5.1.3
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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DEFINITION Sequence 2 from Patent WO0128582.
ACCESSION AX119833
VERSION AX119833.1 GI:14036593
KEYWORDS human.
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ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
TITLE Bumol,T.F. and Cohen,F.J.
JOURNAL Therapeutic applications of flint polypeptides
PATENT: WO 0128582-A 2 26-APR-2001;
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ACCESSION AX167223
VERSION AX167223.1 GI:14596692
KEYWORDS human.
SOURCE
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
TITLE Lu,J. and Witcher,D.R.
JOURNAL Improving stability of flint through o-linked glycosylation
PATENT: WO 0142463-A 2 14-JUN-2001;
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Db 661 CGCGGGCGCTTGCAGCTGAAGCTGGCGGTCTCAGGAGCTCTGGGGGCGCAGGAC 720
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ACCESSION AX375169
VERSION AX375169.1 GI:19169920
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE
1 Micanovic.R. and Wlitcher.D.R.
TITLE Pulmonary administration of flint
JOURNAL Patent: WO 0209668-A 2 07-FEB-2002;
Eli Lilly AND COMPANY (US)
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Db 721 GGGCGCTGTGTGTGCGGCTGTGAGGCGCTGCGCGCTGCGCAGGATGCCGGGCTGAG 780
Qy 261 ArgSerValArgGluArgPheLeuProValHis 271
Db 781 CGAGCGCTCCGTGAGCGCTTCTCCTGTGAC 813

RESULT 4
AF134240 903 bp mRNA linear PRI 11-MAY-1999
LOCUS AF134240
DEFINITION Homo sapiens tumor necrosis factor receptor homolog (TR6) mRNA,
complete cds.
ACCESSION AF134240
VERSION AF134240.1 GI:4768938
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1 (bases 1 to 903)
YU,K.Y., KWON,B., NI,J., ZHAI,Y., EBNER,R. and KWON,B.S.
TITLE A newly identified member of tumor necrosis factor receptor
superfamily (TR6) suppresses LIGHT-mediated apoptosis
JOURNAL J. Biol. Chem. 274 (20), 13733-13736 (1999)
MEDLINE 99253915
PUBMED 10318773
REFERENCE 2 (bases 1 to 903)
KWON,B.S. and YU,K.Y.
TITLE Direct Submission
JOURNAL Submitted (10-MAR-1999) Micro/ImmunoI, Indiana University, 635
Barnhill Drive, Indianapolis, IN 46202, USA
FEATURES
source location/Qualifiers
1..903

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ORIGIN

Alignment Scores:
Pred. No.: 4,27e-64 Length: 903
Score: 1491.00 Matches: 271
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

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QY 21 AlaGlnCysProGlyThrPheValGlnArgProCysArgArgAspSerProThrThr 40
Db 148 GCCAGTGCCCCCAGGACCTTTTGACGCGCGCTGCGCGGACAGACGCCACGACG 207
QY 41 CysGlyProCysProProArgHisTyThrGlnPheTrpAsnTyrlLeuGluArgCysArg 60
Db 208 TGTGGCCCGTGTCCACCGGCCACTACACCGACCTTCTGGAACCTACCTGGAGCGCTCCCG 267
QY 61 TyrCysAsnValLeuGluArgGluGluGluAlaArgAlaCysHisAlaThrHis 80
Db 268 TACTGCAACGCTCTCTCGCGGGAGCGTGAGGAGGAGGACCGGCTTGGCCACGCCAC 327
QY 81 AsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHis 100
Db 328 AACCGTGCTGCGCGTCCCGCACCGGCTTCTTCGCGACGCTGTTCTGCTTGGAGCAC 387
QY 101 AlaSerCysProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGln 120
Db 388 GCATCTGTCTACCTGGTGGCGGCGTATTGCCCGGGACCCCGGACGACGACGACG 447
QY 121 CysGlnProCysProGlyThrPheSerAlaSerSerSerSerSerGluGlnCysGln 140
Db 448 TGGACCGCGTCCCGCCAGGACCTTCTCAGCGAGCAGCTCCAGCTCAGAGCAGTCCG 507
QY 141 ProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerHis 160
Db 508 CCCACCGCAACTGCACCGGCTTGGCGCTTGGCGCTTCAATGTCCAGGCTTCTCCCTCC 567
QY 161 AspThrLeuCysThrSerCysThrGlyPheProLeuSerThrArgValProGlyAlaGlu 180
Db 568 GACACCTGTGCACACGCTGCATGCTTCCCTCAGCACCGAGGTATCAGGAGCTGAG 627
QY 181 GluCysGluArgAlaValIleAspPheValAlaPheGlnAspIleSerIleCysArgLeu 200
Db 628 GAGTGTGAGCGTCCCGCTCATCGACTTGTGGCTTTCAGGACATCTCCATCAAGAGCTG 687
QY 201 GlnArgLeuGlnAlaLeuGluAlaProGluGlyTrpGlyProThrProArgAlaGly 220
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Db 808 GGGGCGCTGCTGCTGCGCTGCTGAGGCTGCTGCGCTGGCCAGGATGCCGGGCTGGAG 867
QY 261 ArgSerValArgGluArgPheLeuProValHis 271
Db 868 CGAGCGCTCCGAGCGCTTCTCTCTGTCAC 900

RESULT 5
LOCUS AF217794 1048 bp mRNA linear PRI 12-FEB-2000
DEFINITION Homo sapiens M68E mRNA, alternatively spliced, complete cds.
ACCESSION AF217794
VERSION AF217794.1 GI:696262
KEYWORDS
SOURCE
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1048)
AUTHORS Bai,C., Connolly,B., Metzker,M.L., Hilliard,C.A., Liu,X.,
Sandig,V., Soderman,A., Galloway,S.M., Liu,Q., Austin,C.P. and
Caskey,C.T.
Overexpression of M68/Dcr3 in human gastrointestinal tract tumors
independent of gene amplification and its location in a four-gene
cluster
Proc. Natl. Acad. Sci. U.S.A. 97 (3), 1230-1235 (2000)
JOURNAL MEDLINE
PUBMED 1065513
REFERENCE 2 (bases 1 to 1048)
AUTHORS Bai,C.
Direct Submission
TITLE Submitted (21-DEC-1999) WP26A-1000, Merck Research Laboratories,
Summeytown Pike, West Point, PA 19403, USA
JOURNAL
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Location/Qualifiers
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/map="20q13.3"
/cell_type="adenocarcinoma"
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BASE COUNT 160 a 367 c 335 g 186 t
ORIGIN

Alignment Scores:
Pred. No.: 4,97e-64 Length: 1048
Score: 1491.00 Matches: 271
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-936-024-1 (1-271) x AF217794 (1-1048)
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 QY 21 AlaGlnCysPropProGlyTyrPheValGlnArgProCysArgArgAspSerProThrThr 40
 Db 200 GCCCAGTGTCCCGCAGGACCTTTGTGACGCGCGTCCCGCCGAGACGCCCCACGACG 259
 QY 41 CysGlnProCysPropProArgHisTyrThrGlnPheThrPheValGlnArgCysArg 60
 Db 260 TGTGGCCCGTGTCCACCGCGCACTACAGGAGTTCTGGAATCACTGTGAGCGCTGTCCGC 319
 QY 61 TyrCysAsnValLeuCysGlyGlyGluArgGlnGluAlaArgAlaCysHisAlaThrHis 80
 Db 320 TACTGCAACGTCCTCTGTGGGAGGTGAGAGGAGGAGGAGCGGCTGTGCAGCCACCCAC 379
 QY 81 AsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGlnHis 100
 Db 380 AACCGTCCTGCGCTGCGCAGCGGCTTCTTCCGCGCACGCTGTGTTCTGTGAGACAC 439
 QY 101 AlaSerCysPropProGlyValGlyVal11eAlaProGlyThrProSerGlnAsnThrGln 120
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 Db 740 CAGCGCTGCTGCAGGCGCTCGAGGCGCCGAGAGGCTGTGGTCCGACACCAAGGGCGGCG 799
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 Db 800 CGCGCGGCTTGTGAGCTGAGACCTGCTCGGCGGCTCAAGGAGCTCTGCGGGCGCAGGAC 859
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 RESULT 6
 AX082868
 LOCUS AX082868 1055 bp DNA linear PAT 28-FEB-2001
 DEFINITION Sequence 1 from Patent WO0110908.
 ACCESSION AX082868
 VERSION AX082868.1 GI:13184802
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 NCTR3, a member of the tnf-receptor supergene family
 TITLE Heu.H.
 AUTHORS Patent: WO 0110908-A 1 15-FEB-2001;
 JOURNAL Amgen Inc. (US)

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 Alignment Scores:
 Pred. No.: 5e-64 Length: 1055
 Score: 1491.00 Matches: 271
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: Gaps: 0
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 Db 214 GCCCAGTGTCCCGCAGGACCTTTGTGACGCGCGTCCCGCCGAGACGCCCCACGACG 273
 QY 41 CysGlnProCysPropProArgHisTyrThrGlnPheThrPheValGlnArgCysArg 60
 Db 274 TGTGGCCCGTGTCCACCGCGCACTACAGGAGTTCTGGAATCACTGTGAGCGCTGTCCGC 333
 QY 61 TyrCysAsnValLeuCysGlyGlyGluArgGlnGluAlaArgAlaCysHisAlaThrHis 80
 Db 334 TACTGCAACGTCCTCTGTGGGAGCTGAGAGGAGGAGGAGCGGCTGTGCAGCCACCCAC 393
 QY 81 AsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGlnHis 100
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 QY 101 AlaSerCysPropProGlyValGlyVal11eAlaProGlyThrProSerGlnAsnThrGln 120
 Db 454 GCATCGTGTCCACTGTGTGCGGAGGTATGCCCCGCGCACCCCGACGACAGAACACGCGAG 513
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 QY 141 ProHisArgAsnValLeuGlnGlnAlaLeuAsnValProGlySerSerSerHis 160
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Db 934 CGGAGCGTCCGTGAGCGCTTCTCCCTGTGCAC 966

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AX055373
LOCUS AX055373 1114 bp DNA linear PAT 13-JAN-2001
DEFINITION Sequence 3 from Patent WO073452.
ACCESSION AX055373
VERSION AX055373.1 GI:12228659
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1114)
REFERENCE
AUTHORS Ashkenazi,A.J., Baker,K.P., Chan,B., Goddard,A., Godowski,P.J.,
Gurney,A.L., Hebert,C., Henzel,W., Kabakoff,R.C., Shelton,D.L.,
Tumas,D., Watanabe,C.K. and Wood,W.I.
TITLE Compositions and methods for the treatment of immune related
diseases
JOURNAL Patent: WO 0073452-A 3 07-DEC-2000;
Genentech, Inc. (US)
FEATURES
source Location/Qualifiers
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BASE COUNT 188 a 379 c 356 g 191 t
ORIGIN

Alignment Scores:
Pred. No.: 5,28e-64 Length: 1114
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6

US-09-936-024-1 (1-271) x AX055373 (1-1114)

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Qy 61 TyrCysAsnValLeuCysGlyGluArgGluGluAlaArgAlaCysHisAlaThrHis 80
Db 368 TACTGCAACGCTCTCTGCGGGGAGCGTGAGGAGGAGCGGCTTGCCACGCCACCCAC 427
Qy 81 AsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHis 100
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Qy 161 AspThrLeuCysThrSerCysThrGlyPheProLeuSerThrArgValProGlyAlaGlu 180
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RESULT 8
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LOCUS AX056645 1114 bp DNA linear PAT 17-JAN-2001
DEFINITION Sequence 1 from Patent WO0075316.
ACCESSION AX056645
VERSION AX056645.1 GI:12309639
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1114)
REFERENCE
AUTHORS Ashkenazi,A.J., Goddard,A., Gurney,A.L., Hillan,K., Napier,M. and
Wood,W.I.
TITLE Methods and compositions for inhibiting neoplastic cell growth
JOURNAL Patent: WO 0075316-A 1 14-DEC-2000;
Genentech, Inc. (US)
FEATURES
source Location/Qualifiers
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BASE COUNT 188 a 379 c 356 g 191 t
ORIGIN

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Pred. No.: 5,28e-64 Length: 1114
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6

US-09-936-024-1 (1-271) x AX056645 (1-1114)

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Db 428 AACCGTCTCGCGCTGCGCGCACCGGCTTTCTTCGCCACGCTGGTTCTTCTTGGAGCAC 487
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D	b		368	TACTCAACAGTCTCTCTCGCGGGAGCGTGAGAGAGAGGCACGGGCTTTGCCACGCCACCAC	427
O	y		81	AaaAaArgAlaCyArArgCYsaArgThrgLyPhePheNalAhIsAlaGLyPheYsaLeuLunHis	100
D	b		428	AACCGTGGCTGGCGGCGGCAACGGCTTCTTCGGCAGCGTGGTTCTGCTTGAAGCAC	487
O	y		101	AlaserCysProProGlYAlaGlyValIlealProGlYThrProSerGlnAsnThrgIn	120
D	b		488	GCATGCTGTCCACTGTGTCCCGGCGGTATGTCGCCGGGACCCCCAGCCAGAACACGCCAG	547
O	y		121	CysGlnProCysProProGlYThrPheSeralaserSerSerSerSerGlnCysgln	140
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D	b		608	CCCACCCGCACTGCACCGGCGCTGGGCGCTGCCTCAATGTCAGAGGCTCTTCCCTCCAT	667
O	y		161	AspThrLeuCysThrSerCyethrGlyPheProLasrSerThrArgValProGlyAlaGlu	180
D	b		668	GACACCCCTGTGCACAGCTGCACCTGCTTCCCCCTCAGCACAGGSGTACAGAGACTGAG	727
O	y		181	GluCyArgIuaArgAlaValIleaspPheValAlapheGlnAspIleSerIleYsarArgLeu	200
D	b		728	GAGTGTGAGCGTGGCGGTATGATCTTTGTGGCTTCCAGAGCATCTCCATCAAGAGGCTG	787
O	y		201	GlnAArgLeuGlnAlaleuGlnAlaProGluGlyYTTPGlyProThrProArgAlaGly	220
D	b		788	CAGCGGCTGTCTGCAGAGCCCTCGAGGCGCCGAGGAGCTGGGCTGCCACACAAAGGCGGGC	847
O	y		221	ArgAlaAlaleuGlnLeuLYseuArgArgAArgLeuThngLeuLeuGlyValaGlnasp	240
D	b		848	CGCGGGGCTTGTCACACTGAAGCTGGGTGGCGGGCTCACGAGCTCTGGGGGGCGAGGAC	907
O	y		241	GlyAlaLeuLeuValaArgLeuGlnAlaleuArgValAlaArgMetProGlyLeuGlu	260
D	b		908	GGGGGCGTGTCTGTCTGGCTGTCTGCAGGCGGCTGCCCGCTGGCCAGGATGCCGGGCTGGAG	967
O	y		261	ArgSerValaArgGluArgPheLeuProValHis	271
D	b		968	CGGAGCGTCCGTGAGAGCGCTTCTCCCTCGHCAC	1000

RESULT 9

AF104419

LOCUS	AF104419	1114 bp	mRNA	linear	PRI 06-JAN-1999
DEFINITION	Homo sapiens decoy receptor 3 (DCR3)		cDNA	complete cds.	
ACCESSION	AF104419				
VERSION	AF104419.1	GI:4106877			
KEYWORDS					
SOURCE					
ORGANISM	Homo sapiens.				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
	1 (bases 1 to 1114)				
	Pictti,R.M., Marsters,S.A., Lawrence,D.A., Roy,M., Kischkel,F.C.,				
	Dowd,P., Huang,A., Donahue,C.J., Sherwood,S.W., Baldwin,D.T.,				
	Godowski,P.J., Wood,W.I., Gurney,A.L., Hillan,K.J., Cohen,R.L.,				
	Godard,A.D., Bozstein,D. and Ashkenazi,A.				
	Genomic amplification of a decoy receptor for Fas ligand in lung				
	and colon cancer				
JOURNAL	Nature	396 (6712),	699-703	(1998)	
MEDLINE	99087326				
PUBMED	9872321				
REFERENCE	2 (bases 1 to 1114)				
AUTHORS	Pictti,R.M., Marsters,S.A., Lawrence,D.A., Roy,M., Kischkel,F.C.,				
	Dowd,P., Huang,A., Donahue,C.J., Sherwood,S.W., Baldwin,D.T.,				
	Godowski,P.J., Wood,W.I., Gurney,A.L., Hillan,K.J., Cohen,R.L.,				
	Godard,A.D., Bozstein,D. and Ashkenazi,A.				

TITLE Direct Submission
JOURNAL Submitted (04-NOV-1998) Molecular Oncology, Gentech, 1 DNA Way,
San Francisco, CA 94080, USA
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cancer"
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Alignment Scores:
Pred. No.: 5,28e-64 Length: 1114
Score: 1491.00 Matches: 271
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatch: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0
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QY 21 AlAgInCySPProProGIYThrPheValGIuArGPProCYsaTgaTgaSPseProThrThr 40
Db 248 GCCCGTCCCCCGGACACTTGTGTGAGCGGCGGTCCCGCGAGACGCCCGCCACGCG 307
QY 41 CysgIyProCySPProProARHISrTyThrGInPhETPaNIrYrLeuGIuArGysaRg 60
Db 308 TGTGGCCCGGTGCACCGCGCATCAGCGAGTCTTGAACTACTGTGAGCGGTGGCCG 367
QY 61 TyrCYsaEnValIeUcYsGIyGIuArGIuGIuAlaArGAlaCYsHISaIaThrHIS 80
Db 368 TACTCAACAGTCTCTGTGGGGAGGCTAGGAGAGGACGCGGCTTGCACGCCACCCAC 427
QY 81 AsnArGAlaCYsaRgCYsaRgThrGIyPhePheAlaHISaIaGIyPheCYsLeuGIuHIS 100
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QY 101 AlaSerCYsPProProGIYAlaGIYValIleAlaPProGIYThrProSeGIaAsnThrGln 120
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QY 121 CysGIInProCySPProProGIYThrPheSeRaIaSeSeSeSeSeSeSeGIuGIInCYsGln 140
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Qy 181 GluCyGlyArgAlaValIleAspPheValAlaPheGlnAspIleSerIleLysArgLeu 200
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Qy 201 GlnArgLeuGlnAlaLeuGlnAlaProGluGlyTTPGlyProThrProArgAlaGly 220
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Qy 241 GlyAlaLeuValArgLeuGlnAlaLeuArgValAlaArgMetProGlyLeuGlu 260
Db 908 GGGGCGCTCTGCTGGGCTGCTGCAGGCGCTGCGGTGGCCAGGATGCCCGGCTGGAG 967
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RESULT 10
LOCUS BC017065 1125 bp mRNA linear PRI 09-NOV-2001
DEFINITION Homo sapiens, tumor necrosis factor receptor superfamily, member
6b, decoy, clone MGC:9587 IMAGE:3886635, mRNA, complete cds.
ACCESSION BC017065
VERSION BC017065.1 GI:16877637
KEYWORDS MGC.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1125)
Direct Submission
Submitted (05-NOV-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTF/Gazdar
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAC Plate: 22 Row: d Column: 23
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BASE COUNT 200 a 378 c 356 g 191 t
ORIGIN
Alignment Scores: 5,34e-64 Length: 1125
Pred. No.: 1491.00 Matches: 271
Score: 1491.00 Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 100.00% Gaps: 0
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US-09-936-024-1 (1-271) x BC017065 (1-1125)
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Qy 41 CysGlyProCysProProArgHisTyThrGlnPheThrAsnTyLeuGluArgCysArg 60
Db 307 TGTGGCCCGTGTCCACCGGCGCCTACAGCGAGTTCTGGAACTACTGTGAGCGCTGCCGC 366
Qy 61 TyrCysAsnValLeuCysGlyGluArgGluGluAlaArgAlaCysHisAlaThrHis 80
Db 367 TACTCAACGCTCTCTCGGGGAGCGTGAGGAGGAGGACGCGGCTGCCACGCCACCCAC 426
Qy 81 AsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHis 100
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Qy 121 CysGlnProCysProProGlyThrPheSerAlaSerSerSerSerSerGlnCysGln 140
Db 547 TGCCAGCGCTGCCCGCCAGGACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 606
Qy 141 ProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerSerHis 160
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Qy 161 AspThrLeuCysThrSerCysThrGlyPheProLeuSerThrArgValProGlyAlaGlu 180
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Qy 221 ArgAlaLeuGlnLeuLysLeuArgArgLeuThrGluLeuLeuGlyAlaGlnAsp 240
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QY	241	GIYALALEULEValArgLeuleuGlnAlaLeuArgValAlaArgMetProGlyLeuGlu	260
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RESULT 11			
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DEFINITION	Homo sapiens, tumor necrosis factor receptor superfamily, member 6b, decoy, clone MGC:21079 IMAGE:4752507, mRNA, complete cds.		
ACCESSION	BC034349		
VERSION	BC034349.1		
KEYWORDS	MGC.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	1 (bases 1 to 1150)		
TITLE	Strausberg,R.		
JOURNAL	Submitted (02-JUL-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA		
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov		
COMMENT	Contact: MGC help desk Email: cgapbs-remail.nih.gov Tissue Procurement: James Cleaver, M.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINT) DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center Center code: BCM-HGSC Web site: http://www.hgsc.bcm.tmc.edu/cdna/ Contact: amg@bcm.tmc.edu Guanatene, P.H., Garcia, A.M., Lu, X., Huiyk, S.W., Hale, S.M., Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M., Richards, S., Gibbs, R.A.		
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BASE COUNT	222 a 382 c 348 g 198 t		

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Dd	256	GCCAGTGCCCCCGGACACTTTGTGACGGCGCGTCGCCGCGAGACGCCCAAGC	315		
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Dd	316	TGTGGCCGCTGCCACCCGCGCACACGCAAGCATGTTCTGAATCTTAAGGCGCGCG	375		
OY	61	TYRCysAnVallLeuCysGIyGluRgLuGluaIaARGAlaCYHIsalATHrhIS	80		
Dd	376	TACTCAACGTCCTTCTGGCGGAGCGTAGAGAGAGGACAGGCTTGCACCCACAC	435		
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Dd	436	AACCGTGCGTGGCGTGCGGACCGGCTTCTTCCGCGACCGTGTTCTGCTTGAGCAC	495		
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Dd	496	GCATGTGTCCACCTGGTGCGCGCGGTGATTGCCCGGACACCCACAGCAGAACGCGAG	555		
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DEFINITION	Sequence 1 from Patent WO9946376.				
ACCESSION	AX017828				
VERSION	AX017828.1	GI:10042431			
KEYWORDS					

SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1168)
AUTHORS Kroeger,B.
TITLE Receptor from the superfamily of tnt-receptors from the human lung
JOURNAL Patent: WO 9946376-A 1 16-SEP-1999;
BASIS AG (DE); KROEGER BURKHARD (DE)
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BASE COUNT 194 a 392 c 371 g 211 t
ORIGIN
Alignment Scores:
Pred. No.: 5,54e-64 Length: 1168
Score: 1491.00 Matches: 271
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-09-936-024-1 (1-271) x AX017828 (1-1168)
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Db 221 GTGGCAGAAACACCCACCTACCCCTGGCGGACGACAGACGGGAGCGGCTGGTGTGC 280
QY 21 AlaGlnCysProGlyThrPheValGlnArgProCysArgArgAspSerProThrThr 40
Db 281 GCCCAGTGCCTCCCGCAGCACCTTTGTGACGGCGCTGGCGGACAGACGCCCGCAGCAGC 340
QY 41 CysGlyProCysProArgHisTyrThrGlnPheThrAsnTyrLeuGluArgCysArg 60
Db 341 TGTGGCCCGGTGCCCGGCCACTACACGAGTTCTTGGAACTACCTGGAGCGCTGCCGC 400
QY 61 TyrCysAsnValLeuCysGlyGluArgGluGluAlaArgAlaCysHisAlaThrHis 80
Db 401 TACTGCAACGTCTCTGGGGAGCGTGAGGAGGAGGACCGGCTTGCACGCCACCCAC 460
QY 81 AsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHis 100
Db 461 AACCGTGCCTCCCGCAGCACCTTCTCCGACACCTGCTGCTTGTGGAGCAC 520
QY 101 AlaSerCysProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGln 120
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QY 121 CysGlnProCysProGlyThrPheSerAlaSerSerSerSerGluGlnCysGln 140
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QY 161 AspThrLeuCysThrSerCysThrGlyPheProLeuSerThrArgValProGlyAlaGlu 180
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QY 181 GluCysGluArgAlaValIleAspPheValAlaPheGlnAspIleSerIleLysArgLeu 200
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QY 261 ArgSerValArgGluArgPheLeuProValHis 271
Db 1001 CGGAGCGTCCGAGCGCTTCTCCCTGTGCAC 1033
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DEFINITION Sequence 18 from patent US 6297367.
ACCESSION AR171895
VERSION AR171895.1 GI:17910845
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1347)
AUTHORS Tribouley,C.
TITLE Polynucleotide encoding TNPL1
JOURNAL Patent: US 6297367-A 18 OCT-2001;
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Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
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QY 61 TyrCysAsnValLeuCysGlyGluArgGluGluAlaArgAlaCysHisAlaThrHis 80
Db 585 TACTGCAACGTCTCTGGGGAGCGTGAGGAGGAGGACCGGCTTGCACGCCACCCAC 644
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VERSION AF217793.1 GI:6969260
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SOURCE Homo sapiens.
ORGANISM Homo sapiens.
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Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1428)
AUTHORS Bai,C., Comolli,B., Metzker,M.L., Hilliard,C.A., Liu,X.,
Sandig,V., Soderman,A., Galloway,S.M., Liu,Q., Austin,C.P. and
Caskey,C.T.
Overexpression of M68/DCR3 in human gastrointestinal tract tumors
independent of gene amplification and its location in a four-gene
cluster
Proc. Natl. Acad. Sci. U.S.A. 97 (3), 1230-1235 (2000)
JOURNAL MEDLINE 20122600
PUBMED 10655513
2 (bases 1 to 1428)
AUTHORS Bai,C.
Direct Submission
Submitted (21-DEC-1999) WP26A-1000, Merck Research Laboratories,
Summeytown Pike, West Point, PA 19403, USA
JOURNAL TITLE Location/Qualifiers
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BASE COUNT 240 a 500 c 448 g 240 t
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BASE COUNT 963 a 1581 c 1529 g 872 t
ORIGIN

Alignment Scores:
Pred. No.: 2,39e-63 Length: 4945
Score: 1491.00 Matches: 271
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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US-09-936-024-1 (1-271) x AB029011 (1-4945)

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Search completed: January 6, 2003, 12:52:56

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Homo sapiens mRNA for KIAA1088 protein, partial cds.
AB029011
AB029011.2 GI:20521759
Homo sapiens brain cDNA to mRNA, clone_lib:pBluescriptII SK plus
clone:hk02589s1.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Kikuno,R., Nagase,T., Ishikawa,K., Hirose,M., Miyajima,N.,
Tanaka,A., Kotani,H., Nomura,N. and Ohara,O.
Prediction of the coding sequences of unidentified human genes.
XIV. The complete sequences of 100 new cDNA clones from brain which
code for large proteins in vitro
DNA Res. 6 (3), 197-205 (1999)
10470851
2 (bases 1 to 4945)
Ohara,O., Nagase,T. and Kikuno,R.
Direct Submission
Submitted (17-JUN-1999) Osamu Ohara, Kazusa DNA Research Institute,
Laboratory of DNA Technology, Yana 1532-3, Kisarazu, Chiba
292-0812, Japan (E-mail:cdhainfo@kazusa.or.jp, Tel:+81-438-52-3913,
Fax:+81-438-52-3914)
On May 9, 2002 this sequence version replaced gi:5689512:
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derived from hk02589)."

Tue Jan. 7 08:40:16 2003

us-09-936-024-1.p2n.rge

Page 13

Job time : 2909 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 6, 2003, 11:15:33 ; Search time 73 seconds
(without alignments)
764.915 Million cell updates/sec

Title: US-09-936-024-1
Perfect score: 1491
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: SPREMBL_21:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mammal:*
8: sp_mhc:*
9: sp_organelle:*
10: sp_phage:*
11: sp_plant:*
12: sp_rodent:*
13: sp_virus:*
14: sp_vertebrate:*
15: sp_unclassified:*
16: sp_virus:*
17: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	333.5	22.4	459	11	Q62327	Q62327 mus musculus
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6	313.5	21.0	433	11	O912M6	O912M6 ratu
7	287	19.2	651	13	Q98SM6	Q98SM6 gallus gall
8	275	18.4	348	12	O57103	O57103 monkeypox v
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11	270.5	18.1	349	12	O57100	O57100 monkeypox v
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13	268.5	18.0	349	12	O57102	O57102 monkeypox v
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20	260	17.4	349	12	O89098	O89098 variola vir
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22	260	17.4	350	12	O57116	O57116 cowpox viru
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33	253.5	17.0	351	12	O57117	O57117 cowpox viru
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39	244	16.4	283	6	Q9X8Z8	Q9X8Z8 cercopithec
40	230.5	15.5	276	13	Q9DDDD2	Q9DDDD2 gallus gall
41	227	15.2	278	6	Q8SQ34	Q8SQ34 sus scrofa
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DT 01-JUN-2002 (TEMBLrel. 21, Last annotation update)
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OC Proteocephale; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
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RC TISSUE=HEAD KIDNEY;
RA pieguenezuelos O., Secombes C.J.;
RT "Screening a rainbow trout (Oncorhynchus mykiss) cDNA library."
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ15137; CAC43329.1; -
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 3_
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
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RC STRAIN=NOD;
RX MEDLINE=95178848; PubMed=7872884;
RA Powell E.E., Wicker L.S., Peterson L.B., Todd J.A.;
RT "Allelic variation of the type 2 tumor necrosis factor receptor
   gene";
RL Mamm. Genome 5:726-727(1994).
DR EMBL; X76401; CAA53981.1; -.
DR HSSP; P19438; INCF.
DR MGD; MGI:1314883; Tnfrcflb.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 4.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 3.
DR Receptor.
KM Receptor.
FT NON_TER 1 1 S -> T.
FT VARIANT 87 87 T -> I.
FT VARIANT 93 93 T -> I.
FT VARIANT 268 268 S -> F.
FT VARIANT 345 345 S -> F.
FT VARIANT 421 421 Y -> C.
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   |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY 130 SASSSSEOCQPHRNCTALGLALNVPGSSSHDTLCT---SCTGFPPLSTRVPAECERA 185
   ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 157 SDTSTSDVCRPHRICSLA---IPGNASTDAVCAPESPILSAIPRTLVVSQPEPTRSQ 212
   ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY 186 VIDFVAQDISIKRLQQLQALEAPBGKPTP-----RAGRALQLKRRRLTELLAOD 240
   ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 213 PLD---QEGSPQSPILSL-----GSTPIEOSTKGISLPIGLIVGTSI----- 257
   ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY 241 GALLVRLQLA---RVAMPGLERSVRERFLP 269
   |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 258 GLMLGLVNCFTLVQKKKPSCLQDRAKVPHP 290
   |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT 5
088734 PRELIMINARY; PRT; 482 AA.
ID 088734;
AC 088734;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE p80 TNF-alpha receptor.
GN TNFR2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98414512; PubMed=9740674;
RA Hurler B., Segade F., Rodriguez R., Ramos S.S., Iazo P.S.;
RT "The Mouse Tumor Necrosis Factor Receptor 2 Gene: Genomic Structure
   and Characterization of the two Transcripts.";
RL Genomics 52:79-98(1998).
DR EMBL; Y14619; CAA74969.1; -.
DR EMBL; Y14620; CAA74969.1; JOINED.
DR EMBL; Y14621; CAA74969.1; JOINED.
DR EMBL; Y14622; CAA74969.1; JOINED.

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DR EMBL; Y14623; CAA74969.1; JOINED.
DR EMBL; Y14679; CAA74969.1; JOINED.
DR HSSP; P19438; INCF.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 4.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 3.
DR Receptor.
SQ SEQUENCE 482 AA; 51106 MW; 66C15046B48FFB3C CRC64;

Query Match 21.9%; Score 327; DB 11; Length 482;
Best Local Similarity 29.3%; Pred. No. 1.2e-20;
Matches 82; Conservative 43; Mismatches 109; Indels 46; Gaps 10;

QY 17 RLVAOCPPGTFVORPCRR-----DSPTTGCPRRHYTFQFWNYLERCYCNVLGER 69
   ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 52 QMCKACKPPGOYVGHFNCKNTSDTVACADSDTVACADCEASMTYQVWNOFRITCLSCSSCSTD 111
   ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY 70 EEEPARACHATHNRCRCRTGTF-----AHAGF---CLEHASCPPGAGVIAPGTPSONTOCC 122
   ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 112 QVETRACTQONNVCAEGAGRYCALKTHSGSCRCQMRLSKCGPFGVASSRAPNVLCACAPGTF 171
   ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY 123 PCPPGTFASSSSEOCQPHRNCTALGLALNVPGSSSHDTLCT---SCTGFPPLSTRVPG 178
   |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 172 ACAPGTFSDTSTSDVCRPHRICSLA---IPGNASTDAVCAPESPILSAIPRTLVVSQ 227
   ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY 179 AEECEAAVIDFVAQDISIKRLQQLQALEAPBGKPTP-----RAGRALQLKRRRLT 233
   ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 228 PEPTRSQPLD---QEGSPQSPILSL-----GSTPIEOSTKGISLPIGLIVGT 277
   ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY 234 ELIGAQDGLLVRLQLA---RVAMPGLERSVRERFLP 269
   |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 278 SL-----GLMLGLVNCFTLVQKKKPSCLQDRAKVPHP 312
   |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT 6
0912M6 PRELIMINARY; PRT; 433 AA.
ID 0912M6;
AC 0912M6;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Tumor necrosis factor receptor type II (fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxId=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY;
RA Osburg B., Peiser C., Doemling D., Schomburg L., Voigt K., Bickel U.;
RT "TNF-receptors p60 and p80 are constitutively expressed by rat brain
   capillary endothelial cells and participate in TNF-alpha transport
   through the blood-brain barrier.";
RL Submitted (SEP-2001) to the EMBL/Genbank/DBD databases.
DR EMBL; AF420214; AAL16021.1; -.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_2.
DR PROSITE; PS50050; TNFR_NGFR_2; 3.
DR Receptor.
KM Receptor.
FT NON_TER 1 1
FT NON_TER 433 433
SQ SEQUENCE 433 AA; 45723 MW; 75736D835E72CA4A CRC64;

Query Match 21.0%; Score 313.5; DB 11; Length 433;
Best Local Similarity 35.1%; Pred. No. 1.6e-19;
Matches 59; Conservative 29; Mismatches 67; Indels 13; Gaps 4;

QY 17 RLVAOCPPGTFVORPCRDSPPTTCGCPRRHYTFQFWNYLERCYCNVLGEREEARAC 76
   ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 32 QMCKACKPPGOYVGHFNCKNTSDTVACADCAAGMFTYQVWNLHTCLSCSSCSTDQVETHC 91
   ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

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QY 77 HATHNRACRTGFFA----HAG---FCLHASCPGAGVIAPGTPSONTOCQCPGPTG 129
DB 92 TKQNRVCACNADSYCALUHGNCRCMKLSCGPGFGVARSRSTNGNVICSACAPGTF 151
QY 130 SASSSSQCPHRNCTALGLALNVPGSSGSHDTLCTCTGTFPLSTRVP 177
DB 152 SDTSSDVCPRHICSLA----IPGNASTDAVCASES--PTPSAVP 193

RESULT 7
ID Q98SM6 PRELIMINARY; PRT; 651 AA.
AC Q98SM6;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Death receptor 6.
OS Gallus gallus (Chicken).
OC Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1];
RP SEQUENCE FROM N.A.
RA Bridgman J.T., Johnson A.L.;
RT "Expression of DR6 in the ovary.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF349908; AAK29666.2; -.
DR HSP; P19438; INCF.
DR InterPro; IPR000488; Death.
DR InterPro; IPR003975; Shal_channel.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00531; death; 1.
DR Pfam; PF00020; TNFR_c6; 4.
DR PRINTS; PR01497; SHALCHANNEL.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS00017; DEATH_DOMAIN; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE; PS00050; TNFR_NGFR_2; 1.
KW Receptor.
SQ SEQUENCE 651 AA; 71003 MW; BDC95A600DAB2C2A CRC64;

Query Match 19.2%; Score 287; DB 13; Length 651;
Best Local Similarity 33.5%; Pred. No. 5.2e-17;
Matches 54; Conservative 27; Mismatches 80; Indels 0; Gaps 0;

QY 11 DAETGERLVCAQCPGTFVQRPCCRDSPFTTCGCPPRHYTQFWNYLRCRYCNVLCGERE 70
DB 43 DRATNQLICDKCPAGTVSVKHCTSLRECSPCDGTFTKHENGIERCHPKPCBLPM 102
QY 71 EEARACHATHNRACRTGFFAHAGFCLERHASCPPGAGVIAPGTPSONTOCQCPGPTGS 130
DB 103 IEKTHCTALTDRECTLSGTFQINDTCVPTVCPGVGVRKKGKTETEDVRCKPCLRGTF 162
QY 131 ASSSSSQCPHRNCTALGLALNVPGSSGSHDTLCTCTGTFPLSTRVP 171
DB 163 DVPSSVMKCKTYTDCFGKNMVVVRPGTKESDNVCGSPASLP 203

RESULT 8
ID O57103 PRELIMINARY; PRT; 348 AA.
AC O57103;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Tumor necrosis factor receptor II homolog.
OS Monkeypox virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.

Query Match 18.4%; Score 275; DB 12; Length 348;
Best Local Similarity 33.1%; Pred. No. 3e-16;
Matches 59; Conservative 29; Mismatches 82; Indels 8; Gaps 3;

QY 10 RDAETGER-LVCAQCPGTFVQRPCCRDSPFTTCGCPPRHYTQFWNYLRCRYCNVLCGE 68
DB 33 KDNEYRSRLCCLSCPPGTIVASRLCDSKNTQCTPCGSDTFTSHNNHLQACLSCNGRCD 92
QY 69 REEARACHATHNRACRTGTF-----AHAGFCLERHASCPPGAGVIAPGTPSONTOCQ 122
DB 93 NOVETRSCTNTHNRICECSPGYCLLKSGSGCRTCKTKGIGYGV-SGYTSTGDVICS 151
QY 123 PCPPGTFSSASSSEOCOPHRNCTALGLALNVPGSSGSHDTLCTCTGTFPLSTRVP 180
DB 152 PCGPGTISHVSTDKCEPVTSTNFYIDVEINLYPNVDISCTRTTTTGLSEISISTSE 209

RESULT 9
ID O57108 PRELIMINARY; PRT; 348 AA.
AC O57108;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Tumor necrosis factor receptor II homolog.
OS Monkeypox virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10244;
RN [1];
RP SEQUENCE FROM N.A.
RA Loparev V.N., Parsons J.M., Esposito J.J.;
RT "DNA sequence analysis as a criterion for allocation of the
orthopoxviruses to a particular species.";
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U88142; AAB34367.1; -.
DR HSP; O14763; IDOG.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS00050; TNFR_NGFR_2; 2.
KW Receptor.
SQ SEQUENCE 348 AA; 38212 MW; E555979057DEC91F CRC64;

Query Match 18.4%; Score 275; DB 12; Length 348;
Best Local Similarity 33.1%; Pred. No. 3e-16;
Matches 59; Conservative 29; Mismatches 82; Indels 8; Gaps 3;

QY 10 RDAETGER-LVCAQCPGTFVQRPCCRDSPFTTCGCPPRHYTQFWNYLRCRYCNVLCGE 68
DB 33 KDNEYRSRLCCLSCPPGTIVASRLCDSKNTQCTPCGSDTFTSHNNHLQACLSCNGRCD 92

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OX NCBI_TaxID=10244;
RN [1];
RP SEQUENCE FROM N.A.
RA Loparev V.N., Parsons J.M., Esposito J.J.;
RT "DNA sequence analysis as a criterion for allocation of the
orthopoxviruses to a particular species.";
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U87847; AAB34364.1; -.
DR HSP; O14763; IDOG.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS00050; TNFR_NGFR_2; 2.
KW Receptor.
SQ SEQUENCE 348 AA; 38184 MW; 34A5E668B27907B5 CRC64;

Query Match 18.4%; Score 275; DB 12; Length 348;
Best Local Similarity 33.1%; Pred. No. 3e-16;
Matches 59; Conservative 29; Mismatches 82; Indels 8; Gaps 3;

QY 10 RDAETGER-LVCAQCPGTFVQRPCCRDSPFTTCGCPPRHYTQFWNYLRCRYCNVLCGE 68
DB 33 KDNEYRSRLCCLSCPPGTIVASRLCDSKNTQCTPCGSDTFTSHNNHLQACLSCNGRCD 92
QY 69 REEARACHATHNRACRTGTF-----AHAGFCLERHASCPPGAGVIAPGTPSONTOCQ 122
DB 93 NOVETRSCTNTHNRICECSPGYCLLKSGSGCRTCKTKGIGYGV-SGYTSTGDVICS 151
QY 123 PCPPGTFSSASSSEOCOPHRNCTALGLALNVPGSSGSHDTLCTCTGTFPLSTRVP 180
DB 152 PCGPGTISHVSTDKCEPVTSTNFYIDVEINLYPNVDISCTRTTTTGLSEISISTSE 209

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QY 69 REEFARACHATHNACRCRTGFF-----AHAGFCLHASCPRGAGVIAPGTPSONTQO 122
 DB 93 NOYETRSCTNTHNRICGSPGYCLIKSGSCRTCKTGIGYV-SGYSTGVICS 151
 QY 123 PCPPTGFSASSSSSEOCOPHRNCALGALNVPGSSSHDPLCTSCGFPPLSTRVPGA 180
 DB 152 PCGPGYSHVSTSDKCEPVTSNTFNIVDVEINLVPVNDTSCRTTTTGLSEISISTSE 209

RESULT 10

057277 PRELIMINARY; PRT; 348 AA.
 ID 057277;
 AC 057277;
 DT 01-JUN-1998 (TREMBLrel. 06, Created)
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
 DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Tumor necrosis factor receptor II homolog (J2R) (J2L).
 GN CRMB OR J2R OR J2L.
 OS Monkeypox virus.
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Orthopoxvirus.
 NCBI_TaxID=10244;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ZAIRE-1996 / 96-17, AND ZAIRE-1996 / 96-16;
 RA Loparev V.N., Parsons J.M., Esposito J.J.;
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ZAIRE-96-I-16;
 RA MEDLINE=21592287; PubMed=11734207;
 RA Shchelnikov S.N., Totmenin A.V., Babkin I.V., Safonov P.F.,
 RA Ryazankina O.I., Petrov N.A., Gutorov V.V., Uvarova E.A.,
 RA Mikheev M.V., Sisler J.R., Esposito J.J., Jahrling P.B., Moss B.,
 RA Sandakhchiev L.S.;
 RT "Human monkeypox and smallpox viruses: genomic comparison.";
 RL FEBS Lett. 509:66-70 (2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ZAIRE-96-I-16;
 RA Shchelnikov S.N., Totmenin A.V., Safonov P.F., Gutorov V.V.,
 RA Ryazankina O.I., Petrov N.A., Babkin I.V., Uvarova E.A.,
 RA Esposito J.J., Moss B., Sisler J.R., Jahrling P.B., Sandakhchiev L.S.;
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U87841; AAB94378.1; -;
 DR EMBL: AF380138; AAL40648.1; -;
 DR EMBL: AF380138; AAL40640.1; -;
 DR HSSP: O14763; IDOG.
 DR InterPro: IPR001368; TNFR_c6.
 DR Pfam: PF00020; TNFR_c6; 2.
 DR SMART: SM00208; TNFR_2.
 DR PROSITE: PS00652; TNFR_NGFR_1; 2.
 DR PROSITE: PS50050; TNFR_NGFR_2; 2.
 SQ SEQUENCE 348 AA; 38212 MW; 54019521556C2D8F CRC64;

Query Match 18.4%; Score 275; DB 12; Length 348;

Best Local Similarity 33.1%; Pred. No. 3e-16; Mismatches 82; Indels 8; Gaps 3;

QY 10 RDAETGER-LVCAQCPPTGVQPCRRDSEPTTCGPPRRHYTOFWNYLBRCRYCNVLCGE 68
 DB 33 KDNVEYRNRNICLSCSPGTAYASRLCDKNTQCTPCGSDPTFTSHNHILQACLSNGRCDS 92
 QY 69 REEFARACHATHNACRCRTGFF-----AHAGFCLHASCPRGAGVIAPGTPSONTQO 122
 DB 93 NOYETRSCTNTHNRICGSPGYCLIKSGSCRTCKTGIGYV-SGYSTGVICS 151
 QY 123 PCPPTGFSASSSSSEOCOPHRNCALGALNVPGSSSHDPLCTSCGFPPLSTRVPGA 180
 DB 152 PCGPGYSHVSTSDKCEPVTSNTFNIVDVEINLVPVNDTSCRTTTTGLSEISISTSE 209

RESULT 11
 ID 057100 PRELIMINARY; PRT; 349 AA.
 AC 057100;
 DT 01-JUN-1998 (TREMBLrel. 06, Created)
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
 DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Tumor necrosis factor receptor II homolog.
 GN CRMB.
 OS Monkeypox virus.
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Orthopoxvirus.
 NCBI_TaxID=10244;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NIGERIA-1971;
 RA Loparev V.N., Parsons J.M., Esposito J.J.;
 RT "DNA sequence analysis as a criterion for allocation of the
 RT orthopoxviruses to a particular species";
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U87844; AAB94361.1; -;
 DR HSSP: O14763; IDOG.
 DR InterPro: IPR001368; TNFR_c6.
 DR Pfam: PF00020; TNFR_c6; 2.
 DR SMART: SM00208; TNFR_2.
 DR PROSITE: PS00652; TNFR_NGFR_1; 2.
 DR PROSITE: PS50050; TNFR_NGFR_2; 2.
 KM Receptor.
 SQ SEQUENCE 349 AA; 38239 MW; DFEC280D478F2422 CRC64;

Query Match 18.1%; Score 270.5; DB 12; Length 349;
 Best Local Similarity 32.6%; Pred. No. 7.4e-16;
 Matches 59; Conservative 29; Mismatches 80; Indels 13; Gaps 5;

QY 10 RDAETGER-LVCAQCPPTGVQPCRRDSEPTTCGPPRRHYTOFWNYLBRCRYCNVLCGE 68
 DB 33 KDNVEYRNRNICLSCSPGTAYASRLCDKNTQCTPCGSDPTFTSHNHILQACLSNGRCDS 92
 QY 69 REEFARACHATHNACRCRTGFF-----AHAGFCLHASCPRGAGVIAPGTPSONTQO 122
 DB 93 NOYETRSCTNTHNRICGSPGYCLIKSGSCRTCKTGIGYV-SGYSTGVICS 151
 QY 123 PCPPTGFSASSSSSEOCOP---HRNCTALGALNVPGSSSHDPLCTSCGFPPLSTRVPGA 179
 DB 152 PCGPGYSHVSTSDKCEPVTSNTFNIVDVEINL--YVNDTSCRTTTTGLSEISISTS 209
 QY 180 E 180
 DB 210 E 210
 RESULT 12
 ID 057101 PRELIMINARY; PRT; 349 AA.
 AC 057101;
 DT 01-JUN-1998 (TREMBLrel. 06, Created)
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
 DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Tumor necrosis factor receptor II homolog.
 GN CRMB.
 OS Monkeypox virus.
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Orthopoxvirus.
 NCBI_TaxID=10244;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ZAIRE-1977;
 RA Loparev V.N., Parsons J.M., Esposito J.J.;
 RT "DNA sequence analysis as a criterion for allocation of the
 RT orthopoxviruses to a particular species";
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U87845; AAB94362.1; -;
 DR HSSP: O14763; IDOG.

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DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
KW Receptor.
SQ SEQUENCE 349 AA; 38311 MW; 02F65B00CFB858BE CRC64;

Query Match
Best Local Similarity 18.0%; Score 268.5; DB 12; Length 349;
Matches 59; Conservative 29; Mismatches 80; Indels 13; Gaps 5;

QY 10 RDAETGER-LVCAQCPGTFVQRCRRDSPTTCGCPPRHYTQFWNYLERCRYCNVLCGE 68
DB 33 KNEYRSRNLCCLSCPPTGYASRLCDSKTNTQCTPCGSDTFTSHNNHQAQLCSNCRGDS 92
QY 69 REEARACHATHNRACRRTGFF-----AHAGFCLHASCPPGAGVIAPGTPSQNTQCQ 122
DB 93 NOVETRSNTHNRICPCSPGYCLLKSGSCRTCSKTKCGIGYGV-SGYTSTGDIVCS 151
QY 123 PCPPGTFSSSSSEOCQP---HRNCTALGLALNVPGSSSHDITLCTSGTGFPLSTRVPGA 179
DB 152 PCGPGTYSHTSVDKCEPVVTSNTFNYIDVEINL--YPVNDTSCRTTTTGLSEISISTS 209

QY 180 E 180
DB 210 E 210

RESULT 13
O57102 PRELIMINARY; PRT; 349 AA.
AC O57102;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Tumor necrosis factor receptor II homolog.
GN Monkeypox virus.
OS Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10244;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BENIN-1978;
RA Loparev V.N., Parsons J.M., Esposito J.J.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U87846; AAB94363.1; -.
DR EMBL; U87994; AAB94365.1; -.
DR EMBL; U87995; AAB94366.1; -.
DR EMBL; U88143; AAB94368.1; -.
DR HSP; O14763; ID0G.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
DE Tumor necrosis factor receptor II homolog.
GN Monkeypox virus.
OS Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10244;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BENIN-1978;
RA Loparev V.N., Parsons J.M., Esposito J.J.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U87846; AAB94363.1; -.
DR HSP; O14763; ID0G.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
KW Receptor.
SQ SEQUENCE 349 AA; 38308 MW; CBD2C949F994C59C CRC64;

Query Match
Best Local Similarity 18.0%; Score 268.5; DB 12; Length 349;
Matches 59; Conservative 29; Mismatches 80; Indels 13; Gaps 5;

QY 10 RDAETGER-LVCAQCPGTFVQRCRRDSPTTCGCPPRHYTQFWNYLERCRYCNVLCGE 68
DB 33 KNEYRSRNLCCLSCPPTGYASRLCDSKTNTQCTPCGSDTFTSHNNHQAQLCSNCRGDS 92
QY 69 REEARACHATHNRACRRTGFF-----AHAGFCLHASCPPGAGVIAPGTPSQNTQCQ 122
DB 93 NOVETRSNTHNRICPCSPGYCLLKSGSCRTCSKTKCGIGYGV-SGYTSTGDIVCS 151
QY 123 PCPPGTFSSSSSEOCQP---HRNCTALGLALNVPGSSSHDITLCTSGTGFPLSTRVPGA 179
DB 152 PCGPGTYSHTSVDKCEPVVTSNTFNYIDVEINL--YPVNDTSCRTTTTGLSEISISTS 209

QY 180 E 180
DB 210 E 210

RESULT 15
O57099 PRELIMINARY; PRT; 349 AA.
AC O57099;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Tumor necrosis factor receptor II homolog.
GN Monkeypox virus.
OS Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10244;
RN [1]
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DB 152 PCGPGTYSHTSVDKCEPVVTSNTFNYIDVEINL--YPVNDTSCRTTTTGLSEISISTS 209

QY 180 E 180
DB 210 E 210

RESULT 14
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AC O57291;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Tumor necrosis factor receptor II homolog.
GN CRMB.
OS Monkeypox virus.
OS Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10244;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VARIOUS STRAINS;
RA Loparev V.N., Parsons J.M., Esposito J.J.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; U88144; AAB94369.1; -.
DR EMBL; U87842; AAB94359.1; -.
DR EMBL; U87994; AAB94365.1; -.
DR EMBL; U87995; AAB94366.1; -.
DR EMBL; U88143; AAB94368.1; -.
DR HSP; O14763; ID0G.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
DE Tumor necrosis factor receptor II homolog.
SQ SEQUENCE 349 AA; 38295 MW; CBD2C949ED2B8E7C CRC64;

Query Match
Best Local Similarity 18.0%; Score 268.5; DB 12; Length 349;
Matches 59; Conservative 29; Mismatches 80; Indels 13; Gaps 5;

QY 10 RDAETGER-LVCAQCPGTFVQRCRRDSPTTCGCPPRHYTQFWNYLERCRYCNVLCGE 68
DB 33 KNEYRSRNLCCLSCPPTGYASRLCDSKTNTQCTPCGSDTFTSHNNHQAQLCSNCRGDS 92
QY 69 REEARACHATHNRACRRTGFF-----AHAGFCLHASCPPGAGVIAPGTPSQNTQCQ 122
DB 93 NOVETRSNTHNRICPCSPGYCLLKSGSCRTCSKTKCGIGYGV-SGYTSTGDIVCS 151
QY 123 PCPPGTFSSSSSEOCQP---HRNCTALGLALNVPGSSSHDITLCTSGTGFPLSTRVPGA 179
DB 152 PCGPGTYSHTSVDKCEPVVTSNTFNYIDVEINL--YPVNDTSCRTTTTGLSEISISTS 209

QY 180 E 180
DB 210 E 210

RESULT 15
O57099 PRELIMINARY; PRT; 349 AA.
AC O57099;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Tumor necrosis factor receptor II homolog.
GN CRMB.
OS Monkeypox virus.
OS Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10244;
RN [1]
```

RP SEQUENCE FROM N.A.
RC STRAIN=SIERRA LEONE-1970;
RA Loparev V.N., Parsons J.M., Eposito J.J.;
RT "DNA sequence analysis as a criterion for allocation of the
orthopoxviruses to a particular species".
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U87843; AAB94360.1; -.
DR HSSP; O14763; 1D0G.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR SMART; SM00209; TNFR_2.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
KW Receptor.
SQ SEQUENCE 349 AA; 38321 MW; FE449028C933F57 CRC64;

Query Match 17.9%; Score 267.5; DB 12; Length 349;
Best Local Similarity 32.6%; Pred. No. 1,4e-15;
Matches 59; Conservative 28; Mismatches 81; Indels 13; Gaps 5;

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DB 33 KDNVYRNRNLCCLSCEPGTYASRLCDSKTNTQCTPCGSDTFTSHNHLOACLSCNGRCD 92
QY 69 REEBARACHATNNRACRCRTGFPA-----HAGFCLHASCPCGAGVIAPGTPSONTQCQ 122
DB 93 NOVETRSCTNTHNRICGSPGYCLKLGALGCRFCISKTKGIGYV-SGYTSTGDVICS 151
QY 123 PCPPGTSSASSSSSEQCQ---HNC TALGLALNVPSSSHDTLCTSGTFPLSTRVPGA 179
DB 152 PCGGTYSHVSTDKCEPVVTSNTFNVIDVEINL--YVNDTSCTRTTTTGLSESISTS 209
QY 180 E 180
DB 210 E 210

Search completed: January 6, 2003, 11:20:08
Job time : 75 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: January 6, 2003, 11:21:05 ; Search time 1970 Seconds
(without alignments)
2227.907 Million cell updates/sec

Title: US-09-936-024-1
Perfect score: 1491
Sequence: 1 VAETPTYPWRDAETGERLVC.....RVAMPGLERSVREPLFVPH 271

Scoring table: BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-UNITS=bits -STRAT=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=45
-OUTALIGN=200 -THR SCORE=DCT -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-USER=US09936024@cgn2.1.1349 @runat_06012003_111607_12141 -NCPu=6 -ICPU=3
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-NARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-XGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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2: em_estchum.*
3: em_estcin.*
4: em_estmu.*
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6: em_estopl.*
7: em_estro.*
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12: gb_est3.*
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27: em_ges_tod.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	1183	79.3	1118	13	BI821789	BI821789 603035863	BI821789 603035863
2	1147	76.9	863	13	BO687526	BO687526 AGENCOURT	BO687526 AGENCOURT
3	1069	71.7	617	12	BE878908	BE878908 601492609	BE878908 601492609
4	1064	71.4	572	14	BM767535	BM767535 K-EST0050	BM767535 K-EST0050
5	1060	71.1	1037	12	BG679499	BG679499 602627514	BG679499 602627514
6	1055	70.8	1203	13	BM480312	BM480312 AGENCOURT	BM480312 AGENCOURT
7	1034.5	69.4	728	14	BM680786	BM680786 UI-E-E01-	BM680786 UI-E-E01-
8	1020	68.4	679	12	BE878006	BE878006 601489784	BE878006 601489784
9	941.5	63.1	874	12	BF339551	BF339551 602039016	BF339551 602039016
10	866	58.1	554	10	AW464298	AW464298 BP230015A	AW464298 BP230015A
11	865.5	58.0	692	10	AW083241	AW083241 xc07a04.x	AW083241 xc07a04.x
12	836	56.1	588	13	BI838357	BI838357 603083306	BI838357 603083306
13	813	54.5	600	10	AW262121	AW262121 qx31d04.x	AW262121 qx31d04.x
14	793	53.2	605	14	BM767088	BM767088 K-EST0049	BM767088 K-EST0049
15	793	53.2	605	14	BM767418	BM767418 K-EST0049	BM767418 K-EST0049
16	793	53.2	606	14	BM767446	BM767446 K-EST0049	BM767446 K-EST0049
17	788	52.9	568	14	BO019285	BO019285 UI-H-DT1-	BO019285 UI-H-DT1-
18	781	52.4	596	14	BM767064	BM767064 K-EST0049	BM767064 K-EST0049
19	781	52.4	616	14	BM743072	BM743072 K-EST0016	BM743072 K-EST0016
20	769	51.6	486	14	BM831338	BM831338 K-EST0105	BM831338 K-EST0105
21	769	51.6	588	14	BM756087	BM756087 K-EST0034	BM756087 K-EST0034
22	769	51.6	593	14	BM759026	BM759026 K-EST0038	BM759026 K-EST0038
23	725	48.6	551	12	BE879166	BE879166 601486906	BE879166 601486906
24	725	48.6	697	12	BE873766	BE873766 601483915	BE873766 601483915
25	679	45.5	1216	14	BO716334	BO716334 AGENCOURT	BO716334 AGENCOURT
26	676	45.3	384	14	BM738195	BM738195 K-EST0002	BM738195 K-EST0002
27	670	44.9	540	10	AW471440	AW471440 xw59e06.x	AW471440 xw59e06.x
28	653	43.8	514	10	AW662363	AW662363 h125f01.x	AW662363 h125f01.x
29	644	43.2	475	9	AI718743	AI718743 ae95h04.x	AI718743 ae95h04.x
30	633	42.5	524	14	BM833454	BM833454 K-EST0108	BM833454 K-EST0108
31	604	40.5	478	12	BF001490	BF001490 7988h10.x	BF001490 7988h10.x
32	586	39.3	500	14	BM833463	BM833463 K-EST0108	BM833463 K-EST0108
33	584	39.2	515	10	AW083914	AW083914 xc25g02.x	AW083914 xc25g02.x
34	580	38.9	448	10	AW014771	AW014771 UI-H-B10-	AW014771 UI-H-B10-
35	566	38.0	448	14	BM672727	BM672727 UI-E-CO-	BM672727 UI-E-CO-
36	546	36.6	445	9	AI857725	AI857725 w121a08.x	AI857725 w121a08.x
37	523	35.1	453	10	AW204999	AW204999 UI-H-B11-	AW204999 UI-H-B11-
38	508	34.1	436	9	AI290210	AI290210 q179g12.x	AI290210 q179g12.x
39	503	33.7	467	9	AA025673	AA025673 ze90h09.s	AA025673 ze90h09.s
40	495	33.2	430	9	AI561219	AI561219 cq27c11.x	AI561219 cq27c11.x
41	495	33.2	452	10	AW771720	AW771720 h171a02.x	AW771720 h171a02.x
42	489	32.8	295	10	AW801019	AW801019 MR3-UM006	AW801019 MR3-UM006
43	487.5	32.7	428	9	AA155701	AA155701 z070e05.r	AA155701 z070e05.r
44	469	31.5	417	10	AW006931	AW006931 wt08b06.x	AW006931 wt08b06.x
45	462	31.0	399	10	AW080544	AW080544 xc33a03.x	AW080544 xc33a03.x

ALIGNMENTS

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LOCUS 603035863F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5176910 5',
DEFINITION mRNA sequence.
ACCESSION BI821789
VERSION BI821789.1 GI:15933339
KEYWORDS EST.
SOURCE Homo sapiens
ORGANISM human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE NIH-MGC http://mgi.mc.nsl.nih.gov/.
1 (bases 1 to 1118)
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE

JOURNAL
COMMENT

Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation by: The I.M.A.G.E. Consortium (LLNL)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11440 row: n column: 15
High quality sequence stop: 758.
Location/Qualifiers

FEATURES

source
1. .1118
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5176910"
/clone_lib="NIH_MGC_115"
/lab_host="DH10B"
/note="Organ: pooled brain, lung, testis; Vector: pCMV-SpORF6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27; 1 male lung, age 27; and 1 male testis, age 69. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH_MGC Library."

BASE COUNT 223 a 377 c 339 g 173 t

ORIGIN

Alignment Scores:
Pred. No.: 9,73e-90 Length: 1118
Score: 1163.00 Matches: 231
Percent Similarity: 98.30% Conservative: 0
Best Local Similarity: 98.30% Mismatches: 3
Query Match: 79.34% Indels: 4
DB: 13 Gaps: 0

US-09-936-024-1 (1-271) x BF821789 (1-1118)

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DB 3 CCCACGACGTGG-CGGTGTCACCGCGCCACTACACGCGAGTTCTGGAATCACTCTGGAG 61
QY 58 -ArgCysArgTyrCysAsnValLeuCysGlyGluArgGluGluAlaAlaCysHi 77
DB 62 CGCTGCGCGTACTGCAACGTCTCTCGGGGAGCGGTGAGGAGGAGCGGGCTTGCCA 121
QY 77 sAlaThrHisAsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAlaGlyPheCy 97
DB 122 CGCCACCACAAACGTCGTCGCGCTCGCGACCGGCTTCTTCGCGACGCTGGTTCGTG 181
QY 97 sLeuGluHisAlaSerCysProProGlyAlaGlyValleAlaProGlyThrProSerGl 117
DB 182 CTTTGAGACACGATCGTGTCCACTGTGCGCGGTGAT-GCCCCGGGACCCCGACCCA 240
QY 117 nAsnThrGlnCysGlnProCysProProGlyThrPheSerAlaSerSerSerSerGl 137
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QY 137 uGlnCysGlnProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValProGlySe 157
DB 301 GCAGTGCAGCCCCACCGCAACTGACGGCCCTGGCGCTCAATGTGCCAGGCTC 360
QY 157 rSerSerHisAspThrLeuCysThrSerCysThrGlyPheProLeuSerThrArgValPr 177
DB 361 TTCCTCCCATGACACCTGTGACACGCTGCACCTGGTTCCTCCCTCAGCAGGTA-CC 419
QY 177 oGlyAlaGluCysGluArgAlaValIleAspPheValAlaPheGlnAspIleSerIl 197
DB 420 AGGAGCTGAGGAGTGTGAGCGTGCCTCATTCGACTTTTGTGGCTTCCAGGACATCTCAT 479

QY 197

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DB 480

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QY 217

oArgAlaGlyArgAlaAlaLeuGlnLeuLysLeuArgArgLeuThrGluLeuLeuGl 237

DB 540

AAGGGCGGCGCGCGCTTGAGCTGAGCTGCGTCGGCGGCTACGGAGTCTCTGGG 599

QY 237

YAlaGlnAspGlyAlaLeuLeuValArgLeuGlnAlaLeuArgValAlaArgMetPr 257

DB 600

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QY 257

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DB 660

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RESULT 2

BO687526

LOCUS

DEFINITION

BO687526

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BO687526 863 bp mRNA linear EST 15-JUL-2002
AGENCOURT_8345883 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6250691
5', mRNA sequence.

BO687526
BO687526.1 GI:21812842

EST.
human.

human.

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NIH-MGC http://mgc.nci.nih.gov/

1. (bases 1 to 863)

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgabbs-remail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCM2394 row: c column: 12

High quality sequence stop: 599.

Location/Qualifiers

1. .863

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:6250691"

/clone_lib="NIH_MGC_110"

/tissue_type="ductal carcinoma, cell line"

/lab_host="DH10B (phage-resistant)"

/note="Organ: pancreas; Vector: pOTB7; Site 1: XhoI;

Site 2: EcoRI; cDNA made by oligo-dT priming

Directionally cloned into EcoRI/XhoI sites using the

following 5' adaptor: GGCACGAG(G). Library constructed by

Ling Hong in the laboratory of Gerald M. Rubin (University

of California, Berkeley) using ZAP-cDNA synthesis kit

(Stratagene) and Superscript II RT (Life Technologies).

Note: this is a NIH_MGC Library."

BASE COUNT 133 a 312 c 276 g 141 t 1 others

ORIGIN

Alignment Scores:

Pred. No.: 7,56e-87 Length: 863

Score: 1147.00 Matches: 220

Percent Similarity: 94.87% Conservative: 2

Best Local Similarity: 94.02% Mismatches: 5

Query Match: 76.93% Indels: 7

DB: 14 Gaps: 2

US-09-936-024-1 (1-271) x BO687526 (1-863)


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Qy 21 AlaGluCysProProGlyThrPheValGlnArgProCysArgArgAspSerProThrThr 40
Db 209 GCCCAATGCCCCCAGGACCTTTGTGCACGGCGCGGCGGACAGACCCCGACGAGC 268
Qy 41 CysGlyProCysProProAArgHisTyThrGlnPheThrAsnTyLeuGluArgCysArg 60
Db 269 TGTGGCCCCGTGTCCACCGCCGACCTACACGAGTTCTGGAACTACCTGAGCCGTGCCCG 328
Qy 61 TyTCysAsnValLeuGlyGlyGluArgGluGluValaArgAlaCysHisAlaThrHis 80
Db 329 TACTGCAACGTCCTCTCGGGGAGCGTGAGAGAGAGGAGGAGGCTTGCGACGCCACCCAC 388
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Db 389 AACCGCCCTGCGCCCTCCGACCGGCGCTTCTTCGCGACGCTGTGCTTGTGAGACAC 448
Qy 101 AlAserCysProProGlyValaGlyValaIleAlaProGlyThrProSerGlnAsnThrGln 120
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Qy 121 CysGlnProCysProProGlyThrPheSerAlaSerSerSerSerSerGluGlnCysGln 140
Db 509 TGCACGCGGCGCCCGCCAGGACCTTCTCAGCCGACGAGTTCCAGCTCAGAGCAGTGCAG 568
Qy 141 ProHisArgAsnCysThr-AlaLeuGlyLeu-AlaLeuAsnValProGlySerSerSerH 160
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Db 629 ATGACAGCTGTGACACGAGCTGACGTGCTTCCCTCAGACCAAGGATACAGAGAGAGCT 688
Qy 180 GluGlu-CysGluArgAlaValaIleAsp-PheValaAlaPheGlnAspIleSerIleCysA 199
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Db 749 AGCTGCAGCGGCTGCTCAGGCGCTCGAGGCGCCGGAAGGCGTGGGGTCCGAACCCAA 808
Qy 218 rglAlaGly---ArgAlaAlaLeuGlnLeuLys 227
Db 809 GGGCGGGGCGCGCCCGGCGCTTGCACACTTGA 840

RESULT 3
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DEFINITION 601492609F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3894794 5',
ACCSSION BE878908
VERSION BE878908.1 GI:10327684
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 617)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaabs-r@mail.nih.gov
Tissue Procurement: DCTD/DTF/Gazdar
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov

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FEATURES
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    /organism="Homo sapiens"
    /db_xref="taxon:9606"
    /clone="IMAGE:3894794"
    /clone_1b="NIH_MGC_69"
    /tissue_type="large cell carcinoma, undifferentiated"
    /lab_host="DH10B (phage-resistant)"
    /note="Organ: lung; Vector: pCMV-SORTS; Site_1: NotI;
    Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
    Average insert size 1.1 kb. Library constructed by Life
    Technologies."
BASE COUNT 91 a 224 c 203 g 99 t
ORIGIN
Alignment Scores:
Pred. No.: 1,85e-80 Length: 617
Score: 1069.00 Matches: 202
Percent Similarity: 98.54% Conservative: 0
Best Local Similarity: 98.54% Mismatches: 3
Query Match: 71.70% Indels: 1
DB: 12 Gaps: 0

US-09-936-024-1 (1-271) x BE878908 (1-617)
Qy 53 TyPAsnTyrlLeuGluArgCysArgTyrcYAsnValLeuGlyGluArgGluGlu 72
Db 4 TGGAACTTACTGAGCGCTGCGCTACTGCAACGTCCTTGTGGGAGCGTGAGAGAG 63
Qy 73 AlArGAlaCysHisAlaThrHisAsnArgAlaCysArgCysArgThyGlyPhePheAla 92
Db 64 GCAAGGCTTGCACGCGCACCAACCGTCTGCGCGCGCGCACCGGCTTCTTCCG 123
Qy 93 HisAlaGlyPheCysLeuGluHisAlaSerCysProProGlyAlaGlyValaIleAlaPro 112
Db 124 CACGCTGTTTGTGCTTGAGACAGCATCGTGCACCTGCTGCGGCGGATGATGCCCG 183
Qy 113 GlyThrProSerGlnAsnThrGlnCysGlnProCysProProGlyThrPheSerAlaSer 132
Db 184 GGCACCCCGCAGAACAGCAGTGCACCGCGTGCACCGCCCGACGACCTTCTCAGCAGC 243
Qy 133 SerSerSerSerGluGlnCysGlnProHisArgAsnCysThrAlaLeuGlyLeuAlaLeu 152
Db 244 AGCTCCAGCTCAGAGAGTGCAGCCCGACCGACTGCAGCGGCTTGGGCTTGCCTC 303
Qy 153 AsnValProGlySerSerSerHisAspThrLeuCysThrSerCysThrGlyPheProLeu 172
Db 304 AATGTCCAGGCTTCTTCTCCATGACACCTGTGACACGCTGCACTGGCTTCCCTC 363
Qy 173 SerThrArgValProGlyAlaGluGluCysGluArgAlaValaIleAspPheValaIlePhe 192
Db 364 AGCACCGAGGTACAGAGAGTGAAGAGTGAAGTGCCTGCTGCTGCTGCTTGCCTTTC 423
Qy 193 GlAspIleSerIleCysArgLeuGlnArgLeuGlnAlaLeuGluAlaProGluGly 212
Db 424 CAGGACATCTTCATCAAGAGGCTGACGGCTGTGAGGCTTCCAGAGGCCCGGAGGGC 483
Qy 213 TyrlTyProThrProArgAlaGlyArgAlaAlaLeuGlnLeuLysLeuArgArgLeu 232
Db 484 TGGGTCTCGACACCAAGGGGGCGCGCGCGCTTGCAGCTGAAGCTGCGCGGCGCTC 543
Qy 233 ThrGluLeuGluGlyAlaGlnAspGlyAlaLeuLeuValaArgLeuGlnAlaLeuArg 252
Db 544 ACGAGGCTCTCTGGGGGCGAGACGGGCGCTGCTGTGTGGTG-CTGACGCGCTTGC 602
Qy 253 ValAlaArgMetPro 257
Db 603 GTGGCAGAGATGCCG 617

RESULT 4
BM767535

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LOCUS BM767535 572 bp mRNA linear EST 04-MAR-2002
 DEFINITION K-EST0050015 S1SNU5s2 Homo sapiens cDNA clone S1SNU5s2-3-E03 5', mRNA sequence.
 ACCESSION BM767535
 VERSION BM767535.1 GI:19097150
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 572)
 AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.
 TITLE 21c Frontier Korean EST Project 2001
 JOURNAL Unpublished (2002)
 COMMENT Contact: Kim YS
 Genome Research Center
 Korea Research Institute of Bioscience & Biotechnology
 52 Boeun-dong Yusong-gu, Daejeon 305-333, South Korea
 Tel: +82-42-860-4470
 Fax: +82-42-860-4409
 Email: yongsung@mail.kribb.re.kr
 Plate: 3 row: E column: 03
 High quality sequence stop: 572.
 Location/Qualifiers
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 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="S1SNU5s2-3-E03"
 /clone_lib="S1SNU5s2"
 /sex="F"
 /tissue_type="Ascites"
 /cell_type="Lymphoblast-like"
 /cell_line="SNU-5"
 /lab_host="Top10F"
 /note="Organ: Stomach; Vector: pcNS; Site 1: EcoRI; Site 2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tobacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoR I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with di-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library. After analyzing and sequencing about 2,000 ~ 3,000 colonies in original cDNA library, the abundant cDNAs were selected and amplified by PCR reaction using vector region primer including T7 promoter as 5' primer and N(dT)14 as 3' primer. The PCR products were used as template for synthesis of biotinylated single stranded RNA by in vitro transcription reaction. The synthesized RNA probes were hybridized with antisense single stranded cDNAs prepared from original library and incubated with avidin-gel. After removing DNA-RNA hybrids by centrifuge, the subtracted cDNA libraries were constructed by transformation of the remaining DNA into competent cells E. coli Top10F with electroporation method."

BASE COUNT 90 a 213 c 174 g 95 t
 ORIGIN

Alignment Scores:
 Pred. No.: 4,43e-80 Length: 572
 Score: 1064.00 Matches: 190
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0

Query Match: 71.36% Indels: 0
 DB: 14 Gaps: 0
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 QY 40 ThrCysGlyProCysProProArgHisTyrThrGlnPheTyrAsnTyrLeuGluAlaGlyCys 59
 |||||
 Db 2 ACGTGTGGCCCGTGTCCACGGGCCACTACACGCGTTCGTGGNACTACTCTGGAGCGCTGC 61
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 QY 60 ArgTyrCysAsnValLeuGluGlyGluArgGluGluGluAlaAargAlaCysHisAlaThr 79
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 Db 62 CGCTACTGCAACGTCCTCTCGGGGAGCGTGAGGAGGAGGACGGGCTTGGCCAGCCACC 121
 |||||
 QY 80 HisAsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGlu 99
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 Db 122 CACAACCGCGCTGCGGCTGCGCACCGGCTTCTTCGCGCACGCTGTTCTCTCTGGAG 181
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 QY 100 HisAlaSerCysProProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThr 119
 |||||
 Db 182 CAGCGATCGTGTCCACTGTGTCCGGCGGTGATTGCCCGGGCACCCCGCCAGCAGACACG 241
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 QY 120 GlnCysGlnProCysProProGlyThrPheSerAlaSerSerSerSerSerGluGlnCys 139
 |||||
 Db 242 CAGTGCAGCGCGTGCCTCCAGGCACCTTCTCAGCCAGCAGGATTCAGCTCAGAGCAGTGC 301
 |||||
 QY 140 GlnProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerSer 159
 |||||
 Db 302 CAGCCCCACCGCAACTGCACGGCCCTGCGGCTGCGCCCTCAATGTGCAGGCTCTTCCTCC 361
 |||||
 QY 160 HisAspThrLeuCysThrSerCysThrGlyPhePheProLeuSerThrArgValProGlyAla 179
 |||||
 Db 362 CATGACACGCTGTGCACAGCTGCCTGCTTCCCTTCCCTCAGCAGGATTCAGGAGCT 421
 |||||
 QY 180 GluGluCysGluArgAlaValIleAspPheValAlaPheGlnAspIleSerIleLysArg 199
 |||||
 Db 422 GAGGAGTGTGAGCGTGCCTCATCGACTTTGTGGCTTTCAGGACATCTCCATCAAGAGG 481
 |||||
 QY 200 LeuGlnArgLeuLeuGlnAlaLeuGluAlaProGluGlyTyrGlyProThrProArgAla 219
 |||||
 Db 482 CTGCAGCGCTGTGTGAGGCGCTTCGAGGCGCCCGAGGGTGGGGTCCGACACCAAGGGCG 541
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 QY 220 GlyArgAlaAlaLeuGlnLeuLysLeuArg 229
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 Db 542 GGCCGCGCGCCTTGCGAGCTGAAGCTGCGT 571
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 BG679499
 LOCUS
 DEFINITION BG679499 1037 bp mRNA linear EST 01-MAY-2001
 mRNA sequence.
 ACCESSION BG679499
 VERSION BG679499.1 GI:13910896
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1037)
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-romail.nih.gov
 Tissue Procurement: James Cleaver, M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLAM10610 row: k column: 04
 High quality sequence stop: 762.
 Location/Qualifiers

Source	1..1037
US-09-9316-024-1 (1-271) x BG679459 (1-1037)	
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ORIGIN	
Alignment Scores:	
Pred. No.:	2,06e-79
Score:	1060.00
Percent Similarity:	86.77%
Best Local Similarity:	84.05%
Query Match:	71.09%
DB:	12
	Gaps: 3
1	Val1a1aGluThrProThyTyrProTPrArgAspAlaGluThrGlyAluArgLeuValCys 20
195	GTGGCAAAACACCACCTACCCCTGGCGGGAAGCAGACAGGGAGCGCTGGTGTGC 254
21	AlaGlnCysProProGlyThrPheValGlnArgProCysArgArgAspSerProThrThr 40
255	GCCAGTGTCCCCCAGGACACTTTGTGTACAGGAGCGGTGCGCCGAGACAGCCCAAGACG 314
41	CysGlyProCysProProArgHisTyrThrGlnPheTyrAsnTyrLeuGluArgCysArg 60
315	TGTGGCCGATGTCCACCGCGCCCACTACAGCAAGTCTGGAACTACTAAGAGCGTGGCCG 374
61	TyrCysAsnValLeuCysGlyGluArgGluGluGluAlaArgAlaCysHisAlaThrHis 80
375	TACTGCACAGCTCTCTCGCGGAGAGCGTGAAGAGAGACAGCGGCTTGGCCACCCACCCAC 434
81	AsnArgAlaCysArgCysArgTnrglyPhePheAlaHisAlaGlyPheCysLeuGluHis 100
435	AACCGTCTTCCGCGCTGCGC-ACCGGCTTTTGGCGAGCGATGTTTGTCTTGAAGAC 493
101	AlaSerCysProProGlyAlaGlyVal11a1aProGlyThrProSerGlnAsnThrGln 120
494	GCACTGATGTCCACCTGTGTGCGGGGTATGTGCCCGGGACCCCAAGCAGAACACGGACG 553
121	CysGlnProCysProProGlyThrPheSerAlaSerSerSerSerSerGluGlnCysGln 140
554	TGCAGCGGTGCCCCCAGGACACCTTCTCAGCAGACAGCTCCAGAGCAGTGGCAG 613
141	ProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerSerHis 160
614	CCCCACGCAACTGCGC-GCCCTGGGCTGTGGCCCTCAATGTGCAGAGCTTTCCTTCAT 672
161	AspThrLeu-CysThrSerCysThr-GlyPheProLeuSerThrArgVal1ProGlyAlaG 180
673	GACACCGCTGTGGACACGAGCTGCACTTGAGCTTCCCTCAGACACAGAGTACAGAGAGCTG 732
180	1uGluCysGlu-ArgAlaVal11leAspPheValAlaPhe-----GlnAsp11Ser11 197
733	AGGAGTGTGAAGCGTGCCTGCATCCGACTTGTGGGCTTCCAGAGGACATCTTCATC 792
197	elYArg-LeuGlnArgLeuLeuGlnAla---LeuGluAlaProGluGlyTyrPgly-Pro 215
793	AAAGAGCTTGCAGGGGCTGTGGCAGGCGCTTCCAGAGGCCCCGAGGGCTGGGGTTCG 852
216	ThrProArgAlaGlyArgAlaAlaLeuGlnLeuLysLeuArgArgArgLeuThrGluLeu 235
853	ACACCAAGGGGGGGCGCGCGCGCTGCAGCTTGAAGCTTGCGTGGCGGGGTCCACGGAGAC 912
236	LeuGlyAla---GlnAspGlyAlaLeuLeuValArgLeu 247

DB	913	TCCGGGGGCGCGCAAGAGGGGCGCTGCTGTCGCGCTG	951
RESULT 6			
LOCUS	BM480312	1203 bp	mRNA linear EST 05-FEB-2002
DEFINITION	AGENCOURT_6424187 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:5491790		
ACCESSION	BM480312		
VERSION	BM480312.1	GI:18529354	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	1 (bases 1 to 1203)		
TITLE	NIH-MGC http://mgc.ncl.nih.gov/ .		
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)		
COMMENT	Unpublished (1999)		
	Contact: Robert Strausberg, Ph.D.		
	Email: cgaps-remail.nih.gov		
	Tissue Procurement: ATCC		
	cDNA Library Preparation: Life Technologies, Inc.		
	DNA Sequencing by: Agencourt Bioscience Corporation		
	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.lnl.gov		
	Plate: LHAM12112 row: n column: 15		
	High quality sequence start: 4		
	High quality sequence stop: 560.		
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	/clone_1b="NIH_MGC_67"		
	/issue_type="retinoblastoma"		
	/lab_host="DH10B (phage-resistant)"		
	/note="Organ: eye; Vector: pCMV-SPOrt6; Site1: NotI; Site2: SalI; Cloned unidirectionally. Primer: oligo dT. Average insert size 1.75 kb. Library constructed by Life Technologies."		
BASE COUNT	202 a 452 c 311 g 238 t		
ORIGIN			
Alignment Scores:			
Pred. No.:	6.58e-79	Length:	1203
Score:	1055.00	Matches:	205
Percent Similarity:	78.65%	Conservative:	23
Best Local Similarity:	76.78%	Mismatches:	35
Query Match:	70.76%	Indels:	35
DB:	13	Gaps:	5
US-09-936-024-1 (1-271) x BM480312 (1-1203)			
Oy	1	Vala	1
Db	193	GTGCGAGAAACACCACCTACCTCCCTGGCGGACGACAGACAGAGGAGCGAGCGCTGCTGTC	252
Oy	21	Ala	1
Db	253	GCCGAGTCCCGCCGACGACCTTGTGTGAGGCGCGTGGCGCGAGACAGCCCGACGACG	312
Oy	41	Cys	1
Db	313	TGTGCGCCGCTGCCACCGCGCCACTACACGAGTTCTGGACTCTCGAGCGCTGCGCG	372
Oy	61	Tyr	1
Db	373	TACTGCAACGCTCTCTGCGGGGAGCGTGAGAGAGGACGCGGCTTGCCACGCCACCCAC	432
Oy	81	Asn	1

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Db 433 AACCGTGCCTGCCGTCACCGGCTTCTTCGGCAGCGTGTCTTCGTGGAGCAC 492
Qy 101 AlaSerCysProProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGln 120
Db 493 GCATCGTGTCCACCTGTGTCCGGCGTGTATTCGCCCGGGCACCCCGAGCAACACGACG 552
Qy 121 CysGlnProCysProProGlyThrPheSerAlaSerSerSerSerSerGluGlnCysGln 140
Db 553 TGCCAGCGGTGCCCGCCAGGACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 612
Qy 141 ProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerSerHis 160
Db 613 CCCACCGCACTGCACGGCCCTGGGCTTCCCTCAATGTGCCAGGCTTCTTCCTCCAT 672
Qy 161 AspThrLeuCysThrSerCysThrGlyPheProLeuSerThrArgValProGlyAla-G1 180
Db 673 GACACCTGTGCACCCGCTGCACCTGGCTTCCCTCAGCACCAGGATACCAAGAGCTGA 732
Qy 180 uGluCysGluArgAlaValIleAspPheVal---AlaPheGln---AspIleSerIleLy 198
Db 733 GGAGTGTGAGCGTGCCTCCATCCACTTGTGGGCTTTTCCAGGACCTCTTCTCTCAA 792
Qy 198 sArgLeuGlnArgLeuLeu---GlnAlaLeuGluAlaPro----- 210
Db 793 AAGTTGAGCGGCTTCTGTCAGCGCCCTCCAAAGGCCCGGTAAAGCTTGGGTGTCCC 852
Qy 211 -----GluGlyTrpGlyProThrProArg----- 218
Db 853 AACACCTAGGCGCGGACCGGGAGTACCCCTAACCTCATACACTTACCACCCCG 912
Qy 219 -----AlaGlyArgAlaAlaLeuGlnLeuLy 227
Db 913 AATCACACCCACCTCTTTTGGCGCACCAATCCTCTGCGAGTTTCTGCTTTGACGCCCC 972
Qy 227 sLeuArgArgArgLeuThr 233
Db 973 TCTCTC-CGTGCGCTTACA 990

RESULT 7
BM680786/c 728 bp mRNA linear EST 27-FEB-2002
LOCUS UI-E-E01-ajc-j-12-0-UI.s1 UI-E-E01 Homo sapiens cDNA clone
DEFINITION UI-E-E01-ajc-j-12-0-UI 3', mRNA sequence.
ACCESSION BM680786
VERSION BM680786.1 GI:18990682
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 728)
AUTHORS Ronaldo M.F., Lennon, G. and Soares, M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 9704477
COMMENT Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
Seq primer: M13 Forward
POLYA=Yes. Location/Qualifiers
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source

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/clone_lib="UI-E-E01"
/tissue_type="fetal eye"
/dev_stage="fetal"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/note="Organ: eye; Vector: pT73-Pac (Pharmacia) with a
modified polylinker; site 1: EcoR I; site 2: Not I;
UI-E-E01 is a normalized cDNA library containing the
following tissue(s): fetal eye. The library was
constructed according to Bonaldo, Lennon and Soares,
Genome Research, 8:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded cDNA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into pT73-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dt)18 tail. The sequence tag for this library is
CGCGTATACC. This library was created for the program, Gene
Discovery in the Visual System, supported by National Eye
Institute (NEI).
TAG_LIB=UI-E-E01
TAG_TISSUE=human fetal eye
TAG_SEQ=CGCGTATACC"
BASE COUNT 133 a 218 c 248 g 129 t
ORIGIN
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Alignment Scores:

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Pred. No.: 1.85e-77 Length: 728
Score: 1034.50 Matches: 196
Percent Similarity: 98.99% Conservative: 0
Best Local Similarity: 98.99% Mismatches: 1
Query Match: 69.38% Indels: 1
DB: 14 Gaps: 1
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US-09-936-024-1 (1-271) x BM680786 (1-728)

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Db 704 GCTTGACAGCCACCCACACCGTGTCTGCCGTGCCGACCGGCTTCTTCGGCAGCT 645
Qy 95 GlyPheCysLeuGluHisAlaSerCysProProGlyAlaGlyValIleAlaProGlyThr 114
Db 644 GGTTCCTGTTGGAGCACGATCGTGCACCTGTGGTGGCGGTGATTGCCCCGGCACCC 595
Qy 115 ProSerGlnAsnThrGlnCysGlnProCysProProGlyThrPheSerAlaSerSer 134
Db 584 CCAGCCAGAACACGACGAGTCCAGCCGCTGCCCGCCAGGACCTTCTCAGCAGCAGCTCC 525
Qy 135 SerSerGluGlnCysGlnProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnVal 154
Db 524 AGCTCAGAGCAGTGCAGAGCCACCCACCACTGCACGCGCCCTGGGCGCTGCCCTCAATGTG 465
Qy 155 ProGlySerSerSerHisAspThrLeuCysThrSerCysThrGlyPheProLeuSerThr 174
Db 464 CCAGGCTTCTCTCCCATGACACCTGTGCACCGAGCTGCACCTGGCTTCCCCCTCAGCACC 405
Qy 175 ArgValPro---GlyAlaGluGluCysGluArgAlaValIleAspPheValAlaPheGln 193
Db 404 AGGTATCCAGCAGGAGCTGAGGAGTGTAGCGCTCCCGCTCATCGACTTGTGGCTTTCCAG 345
Qy 194 AspIleSerIleLeysArgLeuGlnArgLeuLeuGlnAlaLeuGluAlaProGluGlyTrp 213
Db 344 GACATCTCCATCAGAGGCTGCAGCGGCTGTGTCAGCGCCCTCGAGGCCCGCGAGGCTGG 295
Qy 214 GlyProThrProArgAlaGlyArgAlaAlaLeuGlnLeuLeuLeuArgArgLeuThr 233
Db 284 GGTCCGACACCAAGGGCGGCGCGGCTTGCAGCTGAAGCTGCGTGGCGGCTCACG 225
Qy 234 GluLeuLeuGlyAlaGlnAspGlyAlaLeuValArgLeuValArgLeuAlaLeuArgVal 253
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Db      224 GAGCTCTGGGGGCGAGACGCGGGCGCTGCTGCTGCTGAGCGGCTGCCTG 165
Qy      254 AATGMeTProGlyLeuGIuArgSerValArgGIuArgPheLeuProValHis 271
Db      164 GCCAGATCCCGCGGCTGAGAGCGAGCGTCGTAAGCGCTTCTCTGTGCAC 111

RESULT 8
LOCUS    BE878006          679 bp      mRNA      linear      EST 20-OCT-2000
DEFINITION 601489784F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3891908 5',
ACCESSION BE878006
VERSION    BE878006.1 GI:10326782
KEYWORDS   EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 679)
AUTHORS     NIH-MGC http://mgi.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
            Email: cga@bs-remail.nih.gov
            Tissue Procurement: DCTD/DTF/Gazdar
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLM9677 row: h column: 21
            High quality sequence stop: 672.
FEATURES
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        /lab_host="DH10B (phage-resistant)"
        /note="Organ: lung; Vector: pCMV-SORT6; Site 1: NotI;
        Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
        Average insert size 1.1 Kb. Library constructed by Life
        Technologies."
BASE COUNT 113 a 239 c 204 g 123 t
ORIGIN
Alignment Scores:
Pred. No.: 2,82e-76 Length: 679
Score: 1020.00 Matches: 195
Percent Similarity: 99.49% Conservative: 0
Best Local Similarity: 99.49% Mismatches: 1
Query Match: 68.41% Indels: 1
DB: 12 Gaps: 0
US-09-936-024-1 (1-271) x BE878006 (1-679)
Qy      76 CyHisAlaThrHisAsnArgAlaCyArgCyArgThrGlyPhePheAlaHisAlaGly 95
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Qy      96 PheCyLeuGIuHisAlaSerCyPProProGIuAlaGlyValIleAlaProGIuThrPro 115
Db      60 TTCCTGTTGGACACCGCATCGTCCACTGTGGCGGCGGTGATTGCCCGGCGCACCCCC 119
Qy      116 SerGIuAsnThrGlnCyGlnProCySPProProGIuThrPheSerAlaSerSerSer 135
Db      120 ACCGACAAACGACAGTGCACGCGCTGCCCCCGACGACCTTTCACGACGACGCTTCAGC 179
Qy      136 SerGIuGlnCyGlnProHisArgAsnCyThrAlaLeuGIuLeuAlaLeuAsnValPro 155

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Db      180 TCAGACAGTCCAGCCCAACGCAACTGCACGCGCCCTGGGCTGCCTCAATGTGCCA 239
Qy      156 GlySerSerSerHisAspThrLeuCyThrSerCyThrGlyPheProLeuSerThrArg 175
Db      240 GGCTCTCTCCCATACACCTGTGCACCACTGACACTGGCTTCCCTCCACGACGAG 299
Qy      176 ValProGIuAlaGluGluCySGluArgAlaValIleAspPheValAlaPheGlnaspIle 195
Db      300 GTAACGAGAGCTGAGGAGGTGAGGCTGCGCTGCATGACCTTTGTGGCTTTCACGACATC 359
Qy      196 SerIleValArgLeuGlnArgLeuLeuGlnAlaLeuGlnAlaProGIuGlyTyrGIuPro 215
Db      360 TCCATCAAGAGCTGCAGGCGCTGCTGCAGGCGCTTCGAGGCCCGGAGGCGCTGGGCTCCG 419
Qy      216 ThrProArgAlaGlyValArgAlaAlaLeuGlnLeuValysLeuValArgArgLeuThrGluLeu 235
Db      420 AACACAAAGGGGCGGCGCGGCTTTCAGCTGAACTGCTGCGGGGCTCACGGAGCTC 479
Qy      236 LeuGIuAlaGlnAspGIuAlaLeuLeuValArgLeuLeuGlnAlaLeuValAlaArg 255
Db      480 CTGGGGGCGCACAGACGGGCGCTGCTGTCGCGGCTGCTGCAGGCGCTGCGCGCTCCAG 539
Qy      256 MetProGIuLeuGIuArgSerValArgGIuArgPheLeuProValHis 271
Db      540 ATGCCCGGCTGGAGCGGAGCGCTCGTAGCGCTTCTCTGTGTGCAC 587

RESULT 9
LOCUS    BF339551          874 bp      mRNA      linear      EST 22-NOV-2000
DEFINITION 602039016F1 NCI CGAP Brn64 Homo sapiens cDNA clone IMAGE:4186995
ACCESSION BF339551
VERSION    BF339551.1 GI:11286006
KEYWORDS   EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 874)
AUTHORS     NIH-MGC http://mgi.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
            Email: cga@bs-remail.nih.gov
            Tissue Procurement: David N. Louis, M.D.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLM9508 row: p column: 04
            High quality sequence stop: 701.
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        /organism="Homo sapiens"
        /db_xref="taxon:9606"
        /clone="IMAGE:4186995"
        /clone_1ib="NCI CGAP Brn64"
        /tissue_type="gliblastoma with EGFR amplification"
        /lab_host="DH10B (T1 phage-resistant)"
        /note="Organ: brain; Vector: pCMV-SORT6; Site 1: NotI;
        Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
        Average insert size 1.57 Kb. Constructed by Life
        Technologies. Note: this is a NCI CGAP Library."
BASE COUNT 129 a 299 c 301 g 145 t
ORIGIN
Alignment Scores:
Pred. No.: 1.61e-69 Length: 874
Score: 941.50 Matches: 181
Percent Similarity: 82.14% Conservative: 3
Best Local Similarity: 80.80% Mismatches: 27

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Query Match: 63.15% Indels: 14
DB: 12 Gaps: 2

US-09-936-024-1 (1-271) x BF339551 (1-874)

Qy 1 ValAlaGluThrProThrTyrrProTrrArgAspAlaGluThrGlyGluArgLeuValCys 20
Db 185 GTGCAGAAACACCCACTACCCCTGGCGGACGCAGACAGGGAGCGGCTGGTGTGC 244

Qy 21 AlaGlnCysProProGlyThrPheValGlnArgProCysArgArgAspSerProThrThr 40
Db 245 GCCAGTGTCCCGCCAGGACCTTTGTGCAGCGCGCGTGGCCGAGACAGCCACGACG 304

Qy 41 CysGlyProCysProProArgHisTyrrThrGlnPheTrrPentTyrrLeuGluArgCysArg 60
Db 305 TGTGGCCGTGTCCACCGCGCCACTACAGCAGTTCCTGGAACCTACCTGGAGCGGTGCGC 364

Qy 61 TyrCysAsnValLeuCysGlyGluArgGluGluAlaArgAlaCysHisAlaThrHis 80
Db 365 TACTGCAACGTCTCTCGGGGAGCGTGAGGAGGAGCGGGCTTGCCAGCGCCACCCAC 424

Qy 81 AsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHis 100
Db 425 AACCGTGTCCCTGCCGACCGCGCTTCTTCGGCAGCGTGTGTTCTGCTTGGAGCAC 484

Qy 101 AlaSerCysProProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGln 120
Db 485 GCATCGTGTCCACCTGTGTGGCGGTGATTGCCCGGGCACCCCGCAGCAACACGACG 544

Qy 121 CysGlnProCysProProGlyThrPheSerAlaSerSerSerSerGluGlnCysGln 140
Db 545 TGCCAGCGTGTCCCGCCAGGCAACCTTCTCAGCCAGCAGCTCCAGCTCAGACGTGCCAG 604

Qy 141 ProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerSerHis 160
Db 605 CCCACCG-AACTGCAGCGCTGGGGCTTGGCCCTCAATGTGCCAGGCTTCTTCCCAT 663

Qy 161 AspThrLeuCys-ThrSerCysThrGlyPheProLeuSerThrArgValProGlyAlaGln 180
Db 664 GACACCTGTGGCACCAGCTGCTGTTCCCGC---TCAGCACAGGTCACAGAGTTGA 720

Qy 180 uGlu-CysGluArgAlaValIleAspPheValAlaPheGlnAspIleSerIleIysArgL 200
Db 721 TGAAGTGTAGCGTGGCGCTCTCTGAGTTTGTGGCTTTCAGGAGCTCTCCATCAAGAGGT 780

Qy 200 euGlnArgLeuGlnAlaLeuGluAlaProGluGlyTrrGlyProThrProArgAlaG 220
Db 781 GC-----GCGGTGTGGCTTAGGCCCGCGAGGTGG 810

Qy 220 lyArgAla 222
Db 811 GGTCCGCC 818

RESULT 10
AW464298 554 bp mRNA linear EST 24-FEB-2000
LOCUS BP230015A20G11 Soares normalized bovine placenta Bos taurus CDNA
DEFINITION clone BP230015A20G11 5', mRNA sequence.
ACCESSION AW464298
VERSION AW464298.1 GI:7034466
KEYWORDS EST.
SOURCE cow.
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bos.
1 (bases 1 to 554)
Lewin,H.A., Soares,M.B., Rebeiz,M., Pardinas,J., Liu,L. and Larson
,J.H.
TITLE Bovine ESTs
JOURNAL Unpublished (2000)
CONTACT Lewin, H. A.
COMMENT W. M. Keck Center for Comparative and Functional Genomics

```

University of Illinois at Urbana-Champaign
340 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Urbana, IL
61801, USA

Tel: 217 333 5998
Fax: 217 244 5617

Email: h-lewin@uiuc.edu

Funding for cattle EST sequencing was provided by the USDA National
Research Initiative, Animal Genome Resource Grant AG 99-3205-8534
to H. A. Lewin and J. E. Womack. Base Calling/Quality Scores: PHRED

from Washington University Genome Center. Vector Trimmi g:

Cross match from Washington University Genome Center PHRAP suite.
Sequences submitted are vector free and at least 200 bp in length.

PCR Primers

FORWARD: TAATAGGACTCACTATAGG

BACKWARD: ATTAAACCCCTCACTAAAG

Insert Length: 554 Std Error: 0.00

Plate: BP230015A20 row: G column: 11

Seq primer: AGCGGATAACAATTTTCACACAGGA

High quality sequence stop: 554.

Location/Qualifiers

1..554

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/db_xref="taxon:9913"

/clone="BP230015A20G11"

/clone_lib="Soares normalized bovine placenta"

/sex="female"

/lab_host="DH10B"

/note="Organ: placenta; Vector: pT7T3Pac; Site 1: EcoRI;
Site 2: NotI; The cDNA library was contributed by the
Soares laboratory and it was constructed and normalized
as described by Bonaldo, M.F., Lennon, G. and Soares,
M.B. (1996), Genome Research 6(9): 791-806."

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QY	142	HistHgaencySThrAlaLeuGLYleuAlaIleuAenValPProGlySerSerSerHisasp	161
Db	472	CACCGCAACTGCACAGCCCTGGCTGGCTGGCTGCATATGTCCTGCTCCCGCTTACACAGC	531
QY	162	ThrIeuCysThrSerCysThr	168
Db	532	GCCTGTGCACCACTGCACG	552
RESULT 11			
LOCUS	AM083241/c		
DEFINITION	AM083241	692 bp	linear
ACCESSION	AM083241		
KEYWORDS	AM083241.1	GI:6038393	
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Bukatyota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	1 (bases 1 to 692)		
TITLE	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.		
JOURNAL	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index		
COMMENT	Unpublished (1997)		
	Contact: Robert Strausberg, Ph.D.		
	Email: cgapbs-remail.nih.gov		
	Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: Christa Prange, The I.M.A.G.E. Consortium DNA Sequencing by: Washington University Genome Sequencing Center		
	clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: www-bio.lnl.gov/bbrp/image/image.html		
	Seq primer: -40UP from Gldco		
	High quality sequence stop: 414.		
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	/clone="IMAGE:2583534"		
	/clone_id="NCI CGAP Co21"		
	/tissue type="moderately differentiated adenocarcinoma"		
	/lab host="DH10B"		
	/note="Organ: colon; Vector: pCMV-SPORT6, site 1: SalI; site 2: NCI; Cloned unidirectionally. Primer: Oligo dT. Normalized to Cot >500. Average insert size 1.04kb. Normalized version of NCI CGAP Co18. Library constructed by Life Technologies."		
	BASE COUNT	136 a	205 c
	ORIGIN	235 g	115 t
			1 others
Alignment Scores:			
Prid. No.:	3.05e-63	Length:	692
Score:	865.50	Matches:	177
Percent Similarity:	89.95%	Conservative:	2
Best Local Similarity:	88.94%	Mismatches:	18
Query Match:	58.05%	Indels:	3
DB:	10	Gaps:	1
	US-09-936-024-1 (1-271) x AM083241 (1-692)		
QY	74	ArgAlaCysWhaIaThrHisAsnArgAlaCysArgCysArgThrGlyPhePheAlaHis	93
Db	689	CGGTCGCGACGGCTTCCACGACCAACACGCTGCTCCATCGGCGACGGCTTTTTCGACG	630
QY	94	AlaGlyPheCysLeuGlnHisIaIaSerCysPProGlyAlaGlyValIaIaAlaProGly	113
Db	629	CTG---TTTCGCTGAGACACGCATCGTCTCACCTTG-CCGCGCTATATGCCCCGGAC	574
QY	114	ThrProSerGlnAenThrGlnCysGlnProCysPProGlyThrPheSerAlaSerSer	133

Db	Accession	Source	Organism	Reference	Authors	Title	Journal	Comment
Db	573	ACCCAGTCCAGAACACGGCACTGCGACGCCGTCGCCCCCAGGACACTTTCAGCGACGAAGC	514					
Qy	134	SerSerSerGluGlnCySglnProHisArgAsnCySthralaLeuGlyLeuAlaLeuAsn	153					
Db	513	TCCAGCTCAGAGCAGGTGCGACGCCCGCAACGACAGCGGCGTGGGCGTGGCCCTCAAT	454					
Qy	154	ValProGlySerSerSerHisAspThrLeuCySthSerCySthTrgIyPheProLeuSer	173					
Db	453	GTGCCAGGCTCTTCTTCCATGACACCCCTGTGCACCGACTGCACTGGCTTCCCTCAGC	394					
Qy	174	ThrArgValProGlyAlaGluGluCySglnAlaArgAlaValIleAspPheValAlaPheGln	193					
Db	393	ACCGAGGTACCAAGAGCTGAGAGAGTGTGAGGTGTCCTCCGTCATCGACTTGTGGCTTCCAG	334					
Qy	194	AspIleSerIleLeuArgLeuGlnArgLeuGlnAlaLeuGlnAlaProGluGlyTyr	213					
Db	333	GACATCTCCATCAAGAGCTGCGACGCCGCTGCTGACAGCCCTCGAGGCGCCCGAGAGGCTGG	274					
Qy	214	GlyProThrProArgAlaGlyArgAlaAlaLeuGlnLeuIys-LeuArgArgArgLeuTh	233					
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Db	213	GAGAGTCTCTGGGGGCGGACGAGCGGGCGCTGCTGTGGCTGTGCGACGGCGTGGCGGT	154					
Qy	253	AlaArgMetProGlyLeuGlnGluArgSerValArgGluArgPheLeuProValHis	271					
Db	153	GGCCAGCATGCGCGCGGCTCGAGCGCGAGCGTCCGAGCGCTTCTCCCTGTGACAC	99					
RESULT 12								
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DEFINITION	603083306F1 NIH_MGC_120 Homo sapiens cDNA clone IMAGE:5222545 5',							
ACCESSION	B1838357							
VERSION	B1838357.1	GI:15949907						
KEYWORDS	EST.							
SOURCE	human.							
ORGANISM	Homo sapiens							
REFERENCE	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;							
AUTHORS	Mammalia; Euteleostomi; Primates; Catarrhini; Homnidae; Homo.							
TITLE	1 (bases 1 to 588)							
JOURNAL	NIH-MGC http://mgs.nci.nih.gov/.							
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC)							
	Unpublished (1999)							
	Contact: Robert Strausberg, Ph.D.							
	Email: cgapds-remail.nih.gov							
	Tissue Procurement: Life Technologies, Inc.							
	cDNA Library Preparation: Life Technologies, Inc.							
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)							
	DNA Sequencing by: Incyte Genomics, Inc.							
	Clone distribution: MGC clone distribution information can be							
	found through the I.M.A.G.E. Consortium/LNL at:							
	http://image.lnl.gov							
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FEATURES	Location/Qualifiers							
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	/lab_host="DH10B"							
	/note="Organ: pooled pancreas and spleen; Vector:							
	pcwv-SpORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA							
	male. Library is oligo-dT primed and directionally cloned							
	(EcoRV site is destroyed upon cloning). Average insert							
	size 1.5 kb, insert size range 1-2.5 kb. Library is							
	normalized and enriched for full-length clones and was							
	constructed by C. Gubler (Invitrogen). Research Genetics							

tracking code 025. Note: this is a NIH_MGC Library."

BASE COUNT 97 a 224 c 171 g 95 t 1 others

ORIGIN

Alignment Scores:

Pred. No.: 7.6e-61 Length: 588

Score: 836.00 Matches: 145

Percent Similarity: 97.97% Conservative: 0

Best Local Similarity: 97.97% Mismatches: 3

Query Match: 56.07% Indels: 0

DB: 13 Gaps: 0

US-09-936-024-1 (1-271) x BI838357 (1-588)

QY 34 ArgArgAspSerProThrThrCysGlyProCysProProArgHisThrGlnPheTrp 53

Db 1 CGCCGACAGACCCACGAGCGTGGCGCGTGTCCACCGCGCACACACGCGTCTGG 60

QY 54 AsnTyrLeuGluArgCysAgtTyrCysAsnValLeuCysGlyGluArgGluGluAla 73

Db 61 AACTACCTGGAGCGCTGCCGCTACTGCAAGCTCTCTGCGGGAGCGGTGAGGAGGCA 120

QY 74 ArgAlaCysHisAlaThrHisAsnArgAlaCysArgCysArgThrGlyPheAlaHis 93

Db 121 CGGGCTTGGCCAGCCACCCACACCGCGCTGCGCGTGTCCGCGCACCGCTTCTTGGCGCAC 180

QY 94 AlaGlyPheCysLeuGluHisAlaSerCysProProGlyAlaGlyValIleAlaProGly 113

Db 181 GCTGGTTCTTCTGGAGACGCGATCGTGTCCACTGGTGGCGCGTGAATGCCCGGGC 240

QY 114 ThrProSerGlnAsnThrGlnCysGlnProCysProProGlyThrPheSerAlaSer 133

Db 241 ACCCCAGCCAGAACACGCGAGTGCAGCGTGGCGCGCGCGCGCGCGCGCGCGCGTCTCAGCCAGCAGT 300

QY 134 SerSerSerGluGlnCysGlnProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsn 153

Db 301 TCCAGCTCAGAGCAGTGCAGCGCGTGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGTCAAT 360

QY 154 ValProGlySerSerSerHisAspThrLeuCysThrSerCysThrGlyPheProLeuSer 173

Db 361 GTGCCAGGCTCTTCTCTCCATGACAGCTGTGCACAGCTGCATCTGGCTTCCCGCTCAGC 420

QY 174 ThrArgValProGlyAlaGluGlu 181

Db 421 ACCANGGTACCGAGTGCAGCAG 444

RESULT 13

AW262121/c

LOCUS

DEFINITION

600 bp mRNA linear EST 28-DEC-1999

xg31d04.x1 NCI CGAP Lu28 Homo sapiens cDNA clone IMAGE:2752231 3'

similar to TR:095407 DECOY RECEPTOR 3. ;contains TAR1.b1

TAR1 repetitive element ;, mRNA sequence.

AW262121

VERSION

AW262121.1 GI:6638937

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

AUTHORS

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

TUMOR GENE INDEX

Unpublished (1997)

CONTACT: Robert Strausberg, Ph.D.

EMAIL: cgapsb-remail.nih.gov

TISSUE Procurement: Chris Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life

Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The

I.M.A.G.E. Consortium DNA Sequencing by: Washington University

Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LINL at:

www-bio.llnl.gov/bbrp/image/image.html

Possible reversed clone: polyT not found

Seq primer: -400P from Gibco

High quality sequence stop: 410.

Location/Qualifiers

1..600

/organism="Homo sapiens"

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/clone="IMAGE:2752231"

/clone_lib="NCI CGAP Lu28"

/tissue_type="two pooled squamous cell carcinomas"

/lab_host="DH10B"

/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: SalI;

Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt.

Library constructed by Life Technologies."

BASE COUNT 120 a 177 c 199 g 102 t 2 others

ORIGIN

Alignment Scores:

Pred. No.: 6.77e-59 Length: 600

Score: 813.00 Matches: 156

Percent Similarity: 98.12% Conservative: 1

Best Local Similarity: 97.50% Mismatches: 3

Query Match: 54.53% Indels: 0

DB: 10 Gaps: 0

US-09-936-024-1 (1-271) x AW262121 (1-600)

QY 112 ProGlyThrProSerGlnAsnThrGlnCysGlnProCysProProGlyThrPheSerAla 131

Db 600 CCGGGGACCCAGCCAGAACACGCGAGTGCAGCGTGGCGCGCGCGCGCGCGCGTCTCAGCC 541

QY 132 SerSerSerSerSerGluGlnCysGlnProHisArgAsnCysThrAlaLeuGlyLeuAla 151

Db 540 AGCAGCTCCAGCTCAGAGCAGTGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGTGGCC 481

QY 152 LeuAsnValProGlySerSerSerHisAspThrLeuCysThrSerCysThrGlyPhePro 171

Db 480 CTCAATGTGCGAGGCTTCTCTCCATGACACCGCTGCAGCGCGCGCGCGCGCGCGTGGCC 421

QY 172 LeuSerThrArgValProGlyAlaGluGluCysGluArgAlaValIleAspPheValAla 191

Db 420 CTCAGCACCGAGGTACAGAGCTGAGGAGTGTGAGCGTGCAGCGCGCGCGCGCGTGTGGCT 361

QY 192 PheGlnAspIleSerIleLysArgLeuGlnArgLeuGlnAlaLeuGluAlaProGlu 211

Db 360 TTCAGGACATCTCCATCAAGAGCTGCAGCGCGCTGCAGCGCGCGCGCGCGCGTGGAG 301

QY 212 GlyTrpGlyProThrProArgAlaGlyArgAlaLeuGlnLeuLysLeuArgArgArg 231

Db 300 GGCTGGGGTCCGACACCAAGGGCGGCGCGCGCGCGCGCGCGTTCGAGCTGAAGCTGCGTGGCGG 241

QY 232 LeuThrGluLeuLeuGlyAlaGlnAspGlyAlaLeuLeuValArgLeuGlnAlaLeu 251

Db 240 CTCAGGAGCTCTGGGGGCGCAGGACGGGGCGCTGTGGTGGCGCTGTGCAGGCGCTG 181

QY 252 ArgValAlaArgMetProGlyLeuGluArgSerValArgGluArgPheLeuProValHis 271

Db 180 CGGTGGCCAGAGTGGCGGGCTGGAGCGGAGCGTCCGTGAGCGCTTCTCTCCCTGTGCAC 121

RESULT 14

BM767088

LOCUS

DEFINITION

605 bp mRNA linear EST 04-MAR-2002

K-EST0049137 S1SNU5s2 Homo sapiens cDNA clone S1SNU5s2-4-D01 5',

trna sequence.

ACCESSION

BM767088

VERSION

BM767088.1 GI:19096703

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 605)
 AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.
 TITLE 21C Frontier Korean EST Project 2001
 JOURNAL Unpublished (2002)
 COMMENT
 Genome Research Center
 Korea Research Institute of Bioscience & Biotechnology
 52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
 Tel: +82-42-860-4470
 Fax: +82-42-860-4409
 Email: yongsung@mail.kribb.re.kr
 Plate: 4 row: D column: 01
 High quality sequence stop: 605.
 Location/Qualifiers
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 /cell_line="SNU-5"
 /lab_host="Top10F"
 /note="Organ: Stomach; Vector: pcNS; Site_1: EcoRI; Site_2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoR I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library. After analyzing and sequencing about 2,000 ~ 3,000 colonies in original cDNA library, the abundant cDNAs were selected and amplified by PCR reaction using vector region primer including T7 promoter as 5' primer and N(dt)14 as 3' primer. The PCR products were used as template for synthesis of biotinylated single stranded RNA by in vitro transcription reaction. The synthesized RNA probes were hybridized with antisense single stranded cDNAs prepared from original library and incubated with avidin-gel. After removing DNA-RNA hybrids by centrifuge, the subtracted cDNA libraries were constructed by transformation of the remaining DNA into competent cells E. coli Top10F with electroporation method."

BASE COUNT 87 a 221 c 203 g 94 t
 ORIGIN

Alignment Scores:
 Pred. No.: 3.32e-57 Length: 605
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 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 53.19% Indels: 0
 DB: 14 Gaps: 0

US-09-936-024-1 (1-271) x BM767088 (1-605)

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Db 261 GCCCAGAGCCCCCAGGACCTTTGTGCAGCGCCGCGCCGAGACACCCACGACG 320
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 Qy 61 TyrCysAsnValLeuCysGlyGluArgGluGlnGluAlaArgAlaCysHisAlaThrHis 80
 Db 381 TACTGCACCTCTCTCTCGGGAGCGGTGAGAGGAGGACGAGGCTTGCCACGACCCAC 440
 Qy 441 AACCGCGCCGCGCGCTGCCGACCGGCTTCTTGCGCACGCTGTCTTGAGAGAC 500
 Qy 101 AlAserCysProProGlyAlaGlyValIleAlaProGlyThrProserGlnAsnThrGln 120
 Db 501 GCATCGTGTCCACCTGTGGCGCGGTGATTGCCCGGCGACCCCGACGAAACACGACG 560
 Qy 121 CysGlnProCysProProGlyThrPheSerAlaSerSerSerSer 135
 Db 561 TGCCAGCCCGTGGCCCGCCAGGACCTTCTCAGCAGGAGTTCCAGC 605

RESULT 15
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 VERSION BM767418.1 GI:19097033
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 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 605)
 AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.
 TITLE 21C Frontier Korean EST Project 2001
 JOURNAL Unpublished (2002)
 COMMENT
 Genome Research Center
 Korea Research Institute of Bioscience & Biotechnology
 52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
 Tel: +82-42-860-4470
 Fax: +82-42-860-4409
 Email: yongsung@mail.kribb.re.kr
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 /cell_line="SNU-5"
 /lab_host="Top10F"
 /note="Organ: Stomach; Vector: pcNS; Site_1: EcoRI; Site_2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoR I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The

obtained cDNA vectors were used for transformation of competent cells *E. coli* Top10F' by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library. After analyzing and sequencing about 2,000 - 3,000 colonies in original cDNA library, the abundant cDNAs were selected and amplified by PCR reaction using vector region primer including T7 promoter as 5' primer and N(dT)14 as 3' primer. The PCR products were used as template for synthesis of biotinylated single stranded RNA by in vitro transcription reaction. The synthesized RNA probes were hybridized with antisense single stranded cDNAs prepared from original library and incubated with avidin-gel. After removing DNA-RNA hybrids by centrifuge, the subtracted cDNA libraries were constructed by transformation of the remaining DNA into competent cells *E. coli* Top10F' with electroporation method."

BASE COUNT 87 a 221 c 203 g 94 t
ORIGIN

Alignment Scores:
Pred. No.: 3,32e-57 Length: 605
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DB: 14 Gaps: 0

US-09-936-024-1 (1-271) x BM767418 (1-605)

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QY 1 ValAlaGluThrProThrTyrProTyrArgAspAlaGluThrGlyGluArgLeuValCys 20
Db 201 GTGCAGAAACACCCACTACCCCTGGCGGACGCAGACAGAGGAGCGCGTGGTGT 260

QY 21 AlaGlnCysProProGlyThrPheValGlnArgProCysArgArgAspSerProThrThr 40
Db 261 GCCCAGTGCCTCTCTGGCGGAGCGCTTTGTGAGCGCGCGTGGCGGAGACAGCCCCCAGCG 320

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Db 381 TACTGCAACGTCTCTGGCGGAGCGTGAGGAGGAGGACGGGCTTGCCACGCCACCCAC 440

QY 81 AsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHis 100
Db 441 AACCGCGCTGCCGCTGCCGACCGGCTTCTTCGGCAGCGCTGGTTTCTGCTTGGAGCAC 500

QY 101 AlaSerCysProProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGln 120
Db 501 GCATCGTGTCCACTGGTGGCGGCGTGATTGCCCGCGGACCCCGCCAGCCAGACCGCAG 560

QY 121 CysGlnProCysProProGlyThrPheSerAlaSerSerSerSer 135
Db 561 TGCCAGCGGTGCCCGCCCGGAGCACCTTCTCAGCCAGCAGTTCAGC 605

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Search completed: January 6, 2003, 12:04:15
Job time : 1972 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 6, 2003, 11:15:33 ; Search time 37 Seconds
(without alignments)
704.120 Million cell updates/sec

Title: US-09-936-024-1

Perfect score: 1491

Sequence: 1 VAETPTYPWRDAETGERLVC.....RVARMGLERSYVERFLPVH 271

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	340.5	22.8	461	1 A35356	tumor necrosis fac
2	333.5	22.4	459	2 I48854	tumor murine tumour
3	332.5	22.3	474	2 B38634	tumor necrosis fac
4	299.5	20.1	435	2 I54182	tumor necrosis fac
5	289	19.4	651	2 JC7705	death receptor-6 -
6	260	17.4	348	2 T28623	hypothetical prote
7	260	17.4	349	2 D72175	G2R protein - vari
8	260	17.4	349	2 D36858	gene G4R protein -
9	234.5	15.7	325	2 B43692	T2 protein - rabbi
10	215.5	14.5	277	2 I37552	OX40 homolog - hum
11	211.5	14.2	271	2 I21783	OX40 antigen precu
12	211	14.2	277	2 A60773	B-cell activation
13	210.5	14.1	326	1 GQVZML	T2 protein - myxom
14	203	13.6	305	2 A46476	B cell-associated
15	194.5	13.0	272	2 I48700	gene ox40 protein
16	185	12.4	256	2 B32393	T-cell antigen 4-1
17	182	12.2	595	2 A42086	CD30 antigen precu
18	174	11.7	255	2 I38426	lymphocyte activat
19	171.5	11.5	416	1 JN0006	nerve growth facto
20	168	11.3	425	1 A26431	nerve growth facto
21	158	10.6	427	1 GQHUN	nerve growth facto
22	155.5	10.4	337	2 A46484	apoptosis-mediatio
23	148.5	10.0	1574	2 T13954	MEGF6 protein - ra
24	148	9.9	250	1 A49053	CD27 antigen precu
25	147.5	9.9	5376	2 T42215	zonahesin - mouse
26	146.5	9.8	260	1 A46517	CD27 antigen precu
27	145	9.7	335	2 A40036	apoptosis-mediatio
28	143	9.6	1620	2 T27283	hypothetical prote
29	140	9.4	314	2 I37383	FAS soluble protei

30	137.5	9.2	324	2 UC2395	Fas antigen precu
31	135.5	9.1	1299	2 T43251	furin (EC 3.4.21.7
32	135	9.1	2321	2 S78549	notch3 protein - h
33	130.5	8.8	454	1 GOMST1	tumor necrosis fac
34	128.5	8.6	3635	2 T10053	laminin alpha 5 ch
35	127	8.5	1192	2 S69000	laminin gamma 2 ch
36	125.5	8.4	1548	2 S34583	serine proteinase
37	124.5	8.4	1713	2 A55347	adhesive ligand ep
38	123.5	8.3	455	1 GCHUT1	tumor necrosis fac
39	123.5	8.3	493	2 JG5486	membrane glycoprot
40	122.5	8.2	2824	2 T23759	hypothetical prote
41	121	8.1	3106	1 S53868	laminin alpha-2 ch
42	120	8.0	1609	1 MMHUB2	laminin gamma-1 ch
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44	118.5	7.9	461	1 GQRRT1	tumor necrosis fac
45	118.5	7.9	1680	2 A43434	furin (EC 3.4.21.7

ALIGNMENTS

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Tumor necrosis factor receptor 2 precursor [validated] - human
N:Alternate names: 75K tumor necrosis factor receptor; TNF receptor type 2
C:Species: Homo sapiens (man)
C>Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #ext change 08-Dec-2000
C:Accession: A35356; A36475; A48416; A36007; A23666; B35010; I38094
R:Smith, C.A.; Davis, T.; Anderson, D.; Solam, L.; Beckmann, M.P.; Jerzy, R.; Dower, S.K.
Science 248, 1019-1023, 1990
A>Title: A receptor for tumor necrosis factor defines an unusual family of cellular and
A:Reference number: A35356; WUID:90260639; PMID:2160731
A:Accession: A35356
A>Status: preliminary
A:Molecule type: mRNA
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A:Cross-references: GB:M32315; NID:G189185; PIDN:AAA5929.1; PID:G189186
R:Kohno, T.; Brewer, M.T.; Baker, S.L.; Schwartz, P.E.; King, M.W.; Hale, K.K.; Squires,
Proc. Natl. Acad. Sci. U.S.A. 87, 8331-8335, 1990
A>Title: A second tumor necrosis factor receptor gene product can shed a naturally occur
A:Reference number: A36475; WUID:9104591; PMID:2172983
A:Accession: A36475
A>Status: preliminary
A:Molecule type: mRNA
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A:Cross-references: GB:M55994; GB:M89549; NID:G339757; PIDN:AAA36755.1; PID:G339758
R:Dembic, Z.; Loetscher, H.; Gubler, U.; Pan, Y.C.; Lahm, H.W.; Gentz, R.; Brockhaus, M.;
Cytokine 2, 231-237, 1990
A>Title: Two human TNF receptors have similar extracellular, but distinct intracellular,
A:Reference number: A48416; WUID:91370690; PMID:1966549
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A>Status: preliminary
A:Molecule type: protein
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A>Note: sequence extracted from NCBI backbone (NCBIN:63368, NCBIPI:63371)
R:Heller, R.A.; Song, K.; Onach, M.A.; Fischer, W.H.; Chang, D.; Ringold, G.M.
Proc. Natl. Acad. Sci. U.S.A. 87, 6151-6155, 1990
A>Title: Complementary DNA cloning of a receptor for tumor necrosis factor and demonstrat
A:Reference number: A36007; WUID:90349572; PMID:2166946
A:Accession: A36007
A>Status: preliminary
A:Molecule type: mRNA
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R:Loetscher, H.; Schlaeger, E.J.; Lahm, H.W.; Pan, Y.C.E.; Lesslauer, W.; Brockhaus, M.
J. Biol. Chem. 265, 20131-20138, 1990
A>Title: Purification and partial amino acid sequence analysis of two distinct tumor nec
A:Reference number: A23666; WUID:91056048; PMID:2173696
A:Accession: A23666
A>Status: preliminary
A:Molecule type: protein
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QY 77 HATHNRACRRTGFF-----AHAGF---CLEHASCPPGAGVIAPGTPTSQNTOCQPCPGTF 129
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QY 241 GALLVRELLOAL----RVARMPLGLERSVRERFLP 269
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tumor necrosis factor receptor type 2 precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 23-Jul-1999
C;Accession: B38634; A40254; S54816
R;Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen,
Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834, 1991
A;Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis factor
A;Reference number: A38634; MUID:91187885; PMID:1849278
A;Accession: B38634
A;Molecule type: mRNA
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A;Cross-references: GB:M60469; NID:g199827; PIDN:AAA39752.1; PID:g199828
R;Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; Je-
Mol. Cell. Biol. 11, 3020-3026, 1991
A;Title: Molecular cloning and expression of the type 1 and type 2 murine receptors for
A;Reference number: A40254; MUID:91246168; PMID:1645445
A;Accession: A40254
A;Molecule type: mRNA
A;Residues: 1-474 <GOO>
A;Cross-references: GB:M60469; NID:g199827; PIDN:AAA39752.1; PID:g199828
R;Kisnerghis, M.; Fellows, R.; Feldmann, M.; Chernaiovsky, Y.
submitted to the EMBL Data Library, May 1995
A;Description: Characterization of the promoter region of the murine p75-TNF receptor.
A;Reference number: S54816
A;Accession: S54816
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-22 <KIS>
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C;Keywords: cytokine receptor; transmembrane protein
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A:Molecule type: mRNA
A:Residues: 1-651 <BRI>
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QY 77 HATHNACRCRGTFF---AHAGF---CLEHASCPPGAGVIAAGTBSQNTQCCPPGPTF 129
A:Cross-references: GB:AF349908
C:Comment: This receptor, a member of the tumor necrosis factor receptor family, belongs
to the TNF receptor superfamily, class I, member 1, and is involved in the TNF signaling
cascade.
Db 112 TKQNRVCAACEARVYALKTKHSGSCRCMRLSKCGPGFVASSRAPGNVLCACACPGT 171
QY 130 SASSSSECCQPHNCTALGLALNVPGSSSHDTLCT---SCGPFPLSTVPAGEBECERA 185
A:Accession: U00001
A:Molecule type: protein
A:Residues: 1-185
Db 172 SDTSTSDVCRPHRICSTLA---IPGNASTDVADESPSTLSAIPFTLVYSGPEPTRSQ 227
QY 186 VIDFVAFODISIRQLQALAEAPBEGMGPTP-----RAGRAALQTLRRRLTELLGAQD 240
A:Accession: U00001
A:Molecule type: protein
A:Residues: 1-240
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QY 241 GALLVRLQAL---RVARNPGLERSVREPLP 269
A:Accession: U00001
A:Molecule type: protein
A:Residues: 1-269
Db 273 GLIMGLVNCIILVQRKKPSCLQKDAKPHVP 305

RESULT 4

154182
tumor necrosis factor receptor 2-related protein - human
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C:Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 17-Mar-2000
C:Accession: U00001
A:Accession: U00001
R:Baens, M.; Chaffanet, M.; Cassiman, J.J.; Van den Berghe, H.; Marynen, P.
Genomics 16, 214-218, 1993
A:Title: Construction and evaluation of a hncDNA library of human 12p transcribed sequen
A:Reference number: 154182; MUID:93252381; PMID:8486360
A:Accession: U00001
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-435 <RES>
A:Cross-references: GB:U04270; NID:g339761; PIDN:AAA36757.1; PID:g339762
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QY 70 EEARACHATHNRACRCRTGFFAHAGFCLF--H---ASCPPGA-GVIAAGTBSQNTQCC 122
A:Accession: J07705
A:Molecule type: mRNA
A:Residues: 1-651 <BRI>
Db 110 LEEIAPCTSKRKTQRCQCPGFC--AAWALFCTHCELLSDCPGEAEALKEVKGKNNHCV 168
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A:Accession: J07705
A:Molecule type: protein
A:Residues: 1-182
Db 169 PCAGHFGONTSSSARCAQCPHRCENQGLVEAPFIAOSDTTCKAPLR-PLPPEKSGTMLM 227
QY 183 ERAVIDFVAFODIS-----IKRLQALAEAPBEGMGPTPRAG 220
A:Accession: J07705
A:Molecule type: protein
A:Residues: 1-220
Db 228 LAVLLPLAFLLATVPSCTWKSHPSLCRLGSLK--RRQGGEGRPVAG 276

RESULT 5

J07705
death receptor-6 - chicken
C:Species: Gallus gallus (chicken)
C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
C:Accession: J07705
A:Accession: J07705
R:Brigham, J.T.; Bobe, J.; Goetz, F.W.; Johnson, A.L.
Biochem. Biophys. Res. Commun. 284, 1109-1115, 2001
A:Title: Conservation of death receptor-6 in avian and piscine vertebrates.
A:Reference number: J07705; MUID:21308433; PMID:11414698

A:Accession: J07705
A:Molecule type: mRNA
A:Residues: 1-651 <BRI>
A:Cross-references: GB:AF349908
C:Comment: This receptor, a member of the tumor necrosis factor receptor family, belongs
to the TNF receptor superfamily, class I, member 1, and is involved in the TNF signaling
cascade.
A:Gene: dr-6
C:Keywords: ovary
F:1-21/Domain: signal sequence #status predicted <SIG>
F:32-196/Domain: extracellular cysteine-rich, ligand-binding #status predicted <ECU>
F:332-350/Domain: transmembrane #status predicted <TM>
F:410-475/Domain: death domain #status predicted <DED>
F:551-651/Region: conserved cytoplasmic #status predicted

Query Match 19.4%; Score 289; DB 2; Length 651;
Best Local Similarity 33.5%; Pred. No. 2e-14;
Matches 54; Conservative 27; Mismatches 80; Indels 0; Gaps 0;

QY 11 DAETGERLVCAOCPGTFVQRPBDRDPTTCGPPCPRHAYTOFWNYLERCRYCNVLGEE 70
A:Accession: J07705
A:Molecule type: mRNA
A:Residues: 1-651 <BRI>
Db 43 DRATNGELICDKCPAGTYSKHTKSTLRCSPCDGTFTKHENGIERCHPCKKPELPM 102
QY 71 EEARACHATHNRACRCRTGFFAHAGFCLF---H---ASCPPGA-GVIAAGTBSQNTQCCPPGPTFS 130
A:Accession: J07705
A:Molecule type: mRNA
A:Residues: 1-651 <BRI>
Db 103 IEKHTCTALTRDCTCLSGTFQINDCVPTVCVPGVGVKKGTEDEVRCKPCLRGTF 162
QY 131 ASSSSSECCQPHNCTALGLALNVPGSSSHDTLCTGCTGPT 171
A:Accession: J07705
A:Molecule type: protein
A:Residues: 1-171
Db 163 DVPSYWKCKTYDCGKNNVVKFETKESDNYCXSPLSP 203

RESULT 6

T28623
hypothetical protein G2R - variola major virus
C:Species: variola major virus
C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 21-Jul-2000
C:Accession: T28623
R:Massung, R.F.; Esposito, J.J.; Liu, L.I.; Qi, J.; Utteback, T.R.; Knight, J.C.; Aubin,
Nature 366, 748-751, 1993
A:Title: Potential virulence determinants in terminal regions of variola smallpox virus
A:Reference number: Z20488; MUID:94088747; PMID:8264798
A:Accession: T28623
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-348 <NAS>
A:Cross-references: EMBL:122579; NID:g623595; PIDN:AAA60933.1; PID:g439102
A:Experimental source: strain Bangladesh 1975
C:Superfamily: myxoma virus T2 protein; NGF receptor repeat homology

Query Match 17.4%; Score 260; DB 2; Length 348;
Best Local Similarity 32.2%; Pred. No. 1, 7e-12;
Matches 59; Conservative 26; Mismatches 90; Indels 8; Gaps 3;

QY 5 PTYPMWRDAE-TGERLVCAOCPGTFVQRPBDRDPTTCGPPCPRHAYTOFWNYLERCRYCN 63
A:Accession: J07705
A:Molecule type: mRNA
A:Residues: 1-651 <BRI>
Db 27 PNGKCKDTEKRNHCLCSPGETVYASRLDSTNTQCTCGSGTFSRNHPLACISCN 86
QY 64 VLGEREEEARACHATHNRACRCRTGFF---AHAGFCLF---H---ASCPPGA-GVIAAGTBSQNTQCC 117
A:Accession: J07705
A:Molecule type: mRNA
A:Residues: 1-651 <BRI>
Db 87 GRGNSQVETRSNTHNRICECSPGYCYLLKSSGCKACVSGTKGIGYGV-SGHTSVG 145
QY 118 NTQCCPCCPPTGFSASSSSECCQPHNCTALGLALNVPGSSSHDTLCTGCTGPTPLSTRV 177
A:Accession: J07705
A:Molecule type: protein
A:Residues: 1-177
Db 146 DVICSPCGFTGSHVTSADKCEVPNNTPNYIDVELTLYPVADTSCRTTITGLESIL 205
QY 178 GAE 180
A:Accession: J07705
A:Molecule type: protein
A:Residues: 1-180
Db 206 TSE 208

RESULT 7

D72175

G2R protein - variola minor virus (strain Garcia-1966)
C:Species: variola minor virus
C:Date: 24-Nov-1999 #sequence_revision 24-Nov-1999 #text_change 20-Jun-2000
C:Accession: D72175
R:Shchelkunov, S.N.; Totmenin, A.V.; Gutorov, V.V.; Safronov, P.F.; Massung, R.F.; Lopau
submitted to GenBank, March 1998
A:Description: Analysis of the complete coding sequence of DNA of alastrim variola minor
A:Reference number: A72150
A:Accession: D72175
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-349 <SHC>
A:Cross-references: GB:Y16780; NID:G5830555; PIDN:CAB54798.1; PID:G5830759
A:Experimental source: strain Garcia-1966
C:Genetics:
C:Superfamily: myxoma virus T2 protein; NGF receptor repeat homology

Query Match 17.4%; Score 260; DB 2; Length 349;
Best Local Similarity 32.2%; Pred. No. 1.7e-12;
Matches 59; Conservative 26; Mismatches 90; Indels 8; Gaps 3;

QY 5 PTYPWRDAE-TGERLVCAQCPPGTFVQPCRRDSPTTCGPPRHYTFQWNYLRCRYCN 63
DB 28 PNGCKDTEYKRNLCCLSCPPGTYASRLCDSKTNTQCTPCGSGTFTSRNHLPACLSCN 87

QY 64 VLGEREEERACHATHNACRRTGFF-----AHAGFLEHASCPGAGVIAPGTPSQ 117
DB 88 GRCNSNQVETRSCNTTNRICECPGYCLLKGSSGCKACVQTKCGIGYGV-SGHTSVG 146

QY 118 NTOCQCPGPTGTFSSSSSEQCPHRNCTALGLALNVPSSSHDTLCTCTGPPPLSRVP 177
DB 147 DVICSPCGFTYVTSSTDKCEPVNNTFNVIDEITLIPVNDTSCRTTTTGLSESIL 206

QY 178 GAE 180
DB 207 TSE 209

RESULT 8
D36858
gene G4R protein - variola virus
N:Alternate names: B28R protein (COP)
C:Species: variola virus
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 23-Mar-2001
C:Accession: D36858; S46888; S32385; S35987
R:Blinov, V.M.
submitted to GenBank, November 1992
A:Reference number: A36859
A:Accession: D36858
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-349 <BLI>
A:Cross-references: GB:X69198; NID:G456758; PIDN:CAA49137.1; PID:G457087
A:Experimental source: strain India-1967, ssp. major, isolate Ind3
R:Kolykhalov, A.A.; Blinov, V.M.; Gytarov, V.V.; Pozdnyakov, S.G.; Chizhikov, V.E.; Frolo
submitted to the EMBL data Library, April 1992
A:Description: Nucleotide sequence analysis of the region of Variola virus XhoI F O H P
A:Reference number: S46868
A:Accession: S46888
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-349 <COL>
A:Cross-references: EMBL:X67117; NID:G516428; PIDN:CAA47540.1; PID:G516449
A:Experimental source: strain India-1967, isolate Ind3
R:Shchelkunov, S.N.; Blinov, V.M.; Sandakhchiev, L.S.
FEBS Lett. 319, 80-83, 1993
A:Title: Genes of variola and vaccinia viruses necessary to overcome the host protective
A:Reference number: S32385; MUID:93202281; PMID:8384129
A:Accession: S32385
A:Molecule type: DNA
A:Residues: 31-168 <SHC>
A:Cross-references: EMBL:X69198

A:Experimental source: strain India-1967, ssp. major
C:Genetics:
A:Gene: G4R
C:Superfamily: myxoma virus T2 protein; NGF receptor repeat homology
F:32-66/Domain: NGF receptor repeat homology <NGP>
F:68-109/Domain: NGF receptor repeat homology <NGP>
F:110-151/Domain: NGF receptor repeat homology <NG3>

Query Match 17.4%; Score 260; DB 2; Length 349;
Best Local Similarity 32.2%; Pred. No. 1.7e-12;
Matches 59; Conservative 26; Mismatches 90; Indels 8; Gaps 3;

QY 5 PTYPWRDAE-TGERLVCAQCPPGTFVQPCRRDSPTTCGPPRHYTFQWNYLRCRYCN 63
DB 28 PNGCKDTEYKRNLCCLSCPPGTYASRLCDSKTNTQCTPCGSGTFTSRNHLPACLSCN 87

QY 64 VLGEREEERACHATHNACRRTGFF-----AHAGFLEHASCPGAGVIAPGTPSQ 117
DB 88 GRCNSNQVETRSCNTTNRICECPGYCLLKGSSGCKACVQTKCGIGYGV-SGHTSVG 146

QY 118 NTOCQCPGPTGTFSSSSSEQCPHRNCTALGLALNVPSSSHDTLCTCTGPPPLSRVP 177
DB 147 DVICSPCGFTYVTSSTDKCEPVNNTFNVIDEITLIPVNDTSCRTTTTGLSESIL 206

QY 178 GAE 180
DB 207 TSE 209

RESULT 9
B43692
T2 protein - rabbit fibroma virus
C:Species: rabbit fibroma virus, Shope fibroma virus
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C:Accession: B43692
R:Upton, C.; DeLange, A.M.; McFadden, G.
Virology 160, 20-30, 1987
A:Title: Tumorigenic poxviruses: genomic organization and DNA sequence of the telomeric
A:Reference number: A43692; MUID:87321103; PMID:2820128
A:Accession: B43692
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-325 <UPT>
A:Cross-references: GB:M17433
C:Superfamily: myxoma virus T2 protein; NGF receptor repeat homology
F:64-105/Domain: NGF receptor repeat homology <NG2>
F:106-147/Domain: NGF receptor repeat homology <NG3>

Query Match 15.7%; Score 234.5; DB 2; Length 325;
Best Local Similarity 32.9%; Pred. No. 1.4e-10;
Matches 52; Conservative 19; Mismatches 76; Indels 11; Gaps 3;

QY 18 LVCAQCPGPTGTFVQPCRRDSPTTCGPPRHYTFQWNYLRCRYCNVLCGEREEERACH 77
DB 38 LCACASCHPGFYASRLCGPSNTVCSCEGDTFTASTNHAPACVSCRGCTGHLSESQPCD 97

QY 78 ATHNACRRTGFFA-----HAGFLEHASCPGAGVIAPGTPSQNTQCPCPGTFFSA 131
DB 98 RTHDRVNCSTGNYCLLKGQNGCRICAPQTKCPAGYGV-SGHTRAGDTLCEKCPPTYS 156

QY 132 SSSSSSEQCPHRNCTALGLALNVPSSSHDTLCTCTG 169
DB 157 SUSPTERCSTFNYSVGFNL----YPVNETSCTTTAG 190

RESULT 10
I37552
OX40 homolog - human
C:Species: Homo sapiens (man)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 11-Jan-2000
C:Accession: I37552
R:Latza, U.; Durkop, H.; Schnittger, S.; Ringeling, J.; Eitelbach, F.; Hummel, M.; Fona
Eur. J. Immunol. 24, 677-683, 1994

A>Title: The human OX40 homolog: cDNA structure, expression and chromosomal assignment
A:Reference number: 137552; MUID:94170844; PMID:7510240
A:Accession: 137552
A>Status: preliminary; translated from GB/EMBL/DDDBJ
A:Molecule type: mRNA
A:Residues: 1-277 <RES>
A:Cross-references: EMBL:X75962; NID:9472957; PIDN:CAA5376.1; PID:9472958
C:Superfamily: CD27 antigen; NGF receptor repeat homology

Query Match 14.5%; Score 215.5; DB 2; Length 277;
Best Local Similarity 27.0%; Pred. No. 3.2e-09;
Matches 72; Conservative 22; Mismatches 104; Indels 69; Gaps 11;

QY 6 TYPMRAETGERLVCAQCPPTGFVQRPDRSDPTTCGCPPEPRHYTQPMNY--LERCRVCN 63
DB 35 TYPSNR-----CCHCRPGNGVSRCSRSQNTVCRPCGEGFNDVVSSEKPCPCWCN 88
QY 64 VLGEREEERARACHATNRACRCRTGFPAHAGFLEHASCPGAGVIAFGTSPQNTQCP 123
DB 89 LRSQ--SERKQLCTATQDTVCRGAG-----TQPLDSYKPG-----VDCAP 127
QY 124 CPPTGSASSSSSECOCPHNCTALGLALNVPSSSHDTICTS---CTGFPLSTRVSGAE 180
DB 128 CPFGHF--SPGNDQACKPMWNTCTLAGKHTLQPASNSSDAICEDRDPATQPOETQGPAPR 185
QY 181 ECRRAVIDFVAFQDISIKRLQLLEAEQW-----GTPPR-----AGRAALQLRLR 230
DB 186 PL-----TYQPEANFRSTQSGSTRVPEVGGRAVAAILGLG 222
QY 231 RLTELLGADQDALLVRLQLARVAMP 257
DB 223 LVVGLGLPL--AIIALLYLRLRQRLP 247

RESULT 11
S12783
OX40 antigen precursor - rat
N:Alternate names: nerve growth factor receptor homolog
C:Species: Rattus norvegicus (Norway rat)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 05-Nov-1999
C:Accession: S12783; S08036
R:Maillet, S.; Fossuem, S.; Barclay, A.N.
EMBO J. 9, 1063-1068, 1990
A>Title: Characterization of the MRC OX40 antigen of activated CD4 positive T lymphocytes
A:Reference number: S12783; MUID:90214614; PMID:2157591
A:Accession: S12783
A:Molecule type: mRNA
A:Residues: 1-271 <MAL>
A:Cross-references: EMBL:X17037; NID:957830; PIDN:CAA4897.1; PID:957831
C:Superfamily: CD27 antigen; NGF receptor repeat homology
C:Keywords: growth factor receptor; transmembrane protein
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-271/Product: OX40 antigen #status predicted <MAT>
F:211-235/Domain: transmembrane #status predicted <MAT>

Query Match 14.2%; Score 211.5; DB 2; Length 271;
Best Local Similarity 31.5%; Pred. No. 6.4e-09;
Matches 53; Conservative 18; Mismatches 54; Indels 43; Gaps 8;

QY 6 TYPMRAETGERLVCAQCPPTGFVQRPDRSDPTTCGCPPEPRHYTQPMNY--LERCRVCN 63
DB 30 TYD-----SGHK--CCRCQGHGVSRCDHTRDVCHPCBEGFNAENVVDTCQCTQCN 83
QY 64 VLGEREEERARACHATNRACRCRTGFPAHAGFLEHASCPGAGVIAFGT-PSQNT--- 119
DB 84 HRSQ--SELKQNTPTEDTVCQCR-----PQTPRODSHK 117
QY 120 ---QCPGPTGSASSSSSECOCPHNCTALGLALNVPSSSHDTLC 164
DB 118 LGVDVCPCPGHP--SPGSDQACKPMWNTCTLSGKQIRHPSNSLDIVC 163

RESULT 12

A60771
B-cell activation protein CD40 precursor - human
N:Alternate names: B-cell surface antigen Bp50
C:Species: Homo sapiens (man)
C>Date: 03-Jun-1993 #sequence_revision 03-Feb-1994 #text_change 21-Jul-2000
C:Accession: S04460; A60771
R:Stamenkovic, I.; Clark, E.A.; Seed, B.
EMBO J. 8, 1403-1410, 1989
A>Title: A B-lymphocyte activation molecule related to the nerve growth factor receptor
A:Reference number: S04460; MUID:89356608; PMID:2475341
A:Accession: S04460
A:Molecule type: mRNA
A:Residues: 1-277 <STA>
A:Cross-references: EMBL:X60592; NID:929850; PIDN:CAA43045.1; PID:929851
R:Brasch-Anderen, S.; Paulie, S.; Koho, H.; Nike, H.; Aspenstroem, P.; Perlmann, P.
J. Immunol. 142, 562-567, 1989
A>Title: Biochemical characteristics and partial amino acid sequence of the receptor-like
A:Reference number: A60771; MUID:8903941; PMID:2463309
A:Accession: A60771
A:Molecule type: protein
A:Residues: 21-50 <BRA>
A:Experimental source: Burkitt lymphoma cell line Raji
C:Genetics: GDB:CD40
A:Gene: GDB:CD40
A:Cross-references: GDB:215268; OMIM:109535
A:Map position: 20q12-20q13.2
C:Superfamily: CD27 antigen; NGF receptor repeat homology
C:Keywords: B-cell; glycoprotein; phosphoprotein; surface antigen; transmembrane protein
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-277/Product: B-cell activation protein CD40 #status experimental <MAT>
F:21-193/Domain: extracellular #status predicted <EXT>
F:194-215/Domain: transmembrane #status predicted <TM>
F:216-277/Domain: intracellular #status predicted <CIT>
F:153,180/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 14.2%; Score 211; DB 2; Length 277;
Best Local Similarity 30.5%; Pred. No. 7.1e-09;
Matches 46; Conservative 21; Mismatches 76; Indels 8; Gaps 3;

QY 20 CAQCPPTGFVQRPDRSDPTTCGCPPEPRHYTQPMNYLER--RYCNVLGEREEERARAC 76
DB 38 CSIDCPQKXVSDCTFTETETELCPGSESEFLDTWNEETHCHQHKYCDPMLGLVQCKGTS 97
QY 77 HAHNNAACRCRTGFPAH---GFLCHASCPGAGVIAFGTSPQNTQCPGPTGSASS 133
DB 98 ET--DTITCEBGMHCTSEACBSCVLRHSCSPFGVKQIATGVSDTICEPCVPFSNV 155
QY 134 SSSECOCPHNCTALGLALNVPSSSHDTLC 164
DB 156 SAPEKCHPWTSCETKQLVQQAATNKTIVC 186

RESULT 13
GOVZML
T2 protein - myxoma virus (strain Lausanne)
C:Species: myxoma virus
C>Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 18-Jun-1999
C:Accession: A40566
R:Updon, C.; Macen, J.L.; Schreiber, M.; Mcfadden, G.
Virology 184, 370-382, 1991
A>Title: Myxoma virus expresses a secreted protein with homology to the tumor necrosis factor
A:Reference number: A40566; MUID:91335768; PMID:1651597
A:Accession: A40566
A:Molecule type: DNA
A:Residues: 1-326 <UPT>
A:Cross-references: GB:M95181; GB:M37976; NID:9332309; PIDN:AAA46632.1; PID:9332310
C:Superfamily: myxoma virus T2 protein; NGF receptor repeat homology
C:Keywords: glycoprotein
F:64-105/Domain: NGF receptor repeat homology <NG>
F:106-147/Domain: NGF receptor repeat homology <NG3>
F:66,181,205,238/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 14.1%; Score 210.5; DB 1; Length 326;

Best Local Similarity 30.4%; Pred. No. 9.1e-09;
Matches 48; Conservative 19; Mismatches 80; Indels 11; Gaps 3;

QY 18 LVCAQCPPGTFVQPCRRDSTTCGCCPFRHYTQFWNYLERCRYCNVLCGEREEARACH 77
 |||:::|||:
Db 38 LCCTSCPGSVASRLCGLSGSDTVCSCKNETFTASTNHAPACVSCRGRCTCHLSESQCD 97
 |||:

QY 78 ATHNRACRRTGFPA-----HAGFCLEHASCPGGAGVIAGTPSQNTQQCPQPGTFSA 131
 ||||
Db 98 KTRDRVDCSAGNVCLLKGBCRICAPKTKCPAGYG-V-SGHTRTGVDLVLTCKPRYTYS 156

QY 132 SSSSEOCOPHRNCALTALGNALNVPGSSSHDTLCISCTG 169
 :|||:::||:
Db 157 AVSSTETCTGSFNVISVEFNL----YPVNDSCTTTTAG 190

RESULT 14

A46476

B cell-associated surface molecule CD40, long splice form - mouse

C Species: Mus musculus (house mouse)

C Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 17-Nov-2000

C Accession: A46476; A46515

R/Torres, R.M.; Clark, E.A.

J Immunol. 148, 620-626, 1992

A Title: Differential increase of an alternatively polyadenylated mRNA species of murine CD40 gene.

A Reference number: A46476; PMID:92105763; PMID:1370315

A Accession: A46476

A Status: preliminary

A Molecule type: mRNA

A Residues: 1-305 <TOR>

A Cross-references: GB:M83312; NID:g1553058

A Note: sequence extracted from NCBI backbone (NCBIN:75206, NCPIP:75207)

R/Grimaldi, J.C.; Torres, R.; Kozak, C.A.; Chang, R.; Clark, E.A.; Howard, M.; Cockayne, D.

J Immunol. 149, 3921-3926, 1992

A Title: Genomic structure and chromosomal mapping of the murine CD40 gene.

A Reference number: A46515; PMID:93094586; PMID:1281194

A Accession: A46515

A Status: preliminary; not compared with conceptual translation

A Molecule type: nucleic acid

A Residues: 1-287, 'LV' <GRI>

A Cross-references: GB:M83312; NID:g1553058; PIDN:AAB08705.1; PID:g1553059; GB:M94126; NID:g1553059

A Experimental source: BALB/c, liver

A Note: sequence extracted from NCBI backbone (NCPIP:120357)

C Comment: For an alternative splice form, see PIR:A46515.

C Comment: For an alternative splice form, see PIR:A46476.

C Superfamily: CD27 antigen; NGF receptor repeat homology

C Keywords: alternative splicing; transmembrane protein

F: I05-I44/Domain: NGF receptor repeat homology <NGP>

Query Match 13.6%; Score 203; DB 2; Length 305;
Best Local Similarity 31.1%; Pred. No. 3.1e-08;
Matches 47; Conservative 19; Mismatches 77; Indels 8; Gaps 3;

QY 20 CAQCPTGTFFVQPCRDRDPITCCGPCPFRHYTQFWNYLERC---RYCNVLCGEREERAC 76
 |||:::|||:
Db 38 CDLCQPGRSLTSHTALEKTQHPDCSGEGFAQMWRREICHOHRCEPNQGURLVKKEQT- 96
 |||:

QY 77 HATHNRACRRTGFPA--HAGFCLEHASCPGGAGVIAGTPSQNTQQCPQPGTFSSA 133
 ||||
Db 97 -AESTVTCTKEGOHCSTKDCEACAQHPTCLPIFGVMEMATETTDTDVCHPCFPVGFFSNQS 155

QY 134 SSSEOCOPHRNCALTALGNALNPVPGSSSHDTLC 164
 |::|::|:
bb 156 SLFEKYCWTSCEDKNLEVLOKGTOTNWIC 186

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C:Accession: I48700; I48334; S34377
R:Caldrehead, D.M.; Buhlmann, J.E.; van den Eertwegh, A.J.; Claassen, E.; Noelle, R.J.;
J. Immunol. 151, 5261-5271, 1993
A:Title: Cloning of mouse Oxa4: a T cell activation marker that may mediate T-B cell in
A:Reference number: I48700; MUID:94044750; PMID:8228223
A:Accession: I48700
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-272 <RES>
A:Cross-references: EMBL:Z21674; NID:g312827; PIDN:CAA79772.1; PID:g312828
R:Birkeland, M.L.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.A.; Barclay, A.N.
Eur. J. Immunol. 25, 926-930, 1995
A:Title: Gene structure and chromosomal localization of the mouse homologue of rat Oxa4
A:Reference number: I48334; MUID:95255413; PMID:7737295
A:Accession: I48334
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-14, 'G', 16-272 <RES>
A:Cross-references: EMBL:X65214; NID:g732818; PIDN:CAA59476.1; PID:g732819
C:Genetics:
A:Gene: Oxa4
A:Introns: 45/1; 86/1; 122/1; 144/2; 210/1; 250/1
C:Superfamily: CD27 antigen; NGF receptor repeat homology

Query Match      13.0%; Score 194.5; DB 2; Length 272;
Best Local Similarity 30.4%; Pred No. 1.2e-07;
Matches 51; Conservative 16; Mismatches 58; Indels 43; Gaps 8;

Qy      6  TYPWRDAETGRLVCAQCPPTFFVQRCRRDSPTTGCGPPRHYTQFWNY--LERCRCYN 63
      |||      :      :      :      :      :      :      :      :
Db      31  TYP-----SGHK-CRECPQGHGVMSCRDHTRDTLCHPCETGFGYNEAVNYDTCQCTQCN 84
      |||      :      :      :      :      :      :      :      :

Qy      64  VLCGEREERAPACHATHNRACRTGTGFFAHAGFCLHASCPPGAGVIAPGT-PSQNT--- 119
      |||      :      :      :      :      :      :      :      :
Db      85  HRSG--SELKQNCPTQDTVCRCR-----PGTQPRQDSGYK 118
      |||      :      :      :      :      :      :      :      :

Qy      120  ---QCQCPPTGTFSSSSSSSQCPHRNCTALGLALNVPGSSSHDTLC 164
      |||      :      :      :      :      :      :      :      :
Db      119  LGVDCVCPGPHF--SPGNQACFPWNTCTLSGKQTRHPASDSDLDAVC 164
      |||      :      :      :      :      :      :      :      :

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